

Figure 1

Motif 0

human
ce21
EST1
p123

AKFLHNLHLSVYVVELLRSPFFYVTEITTFQXNR
ISEIEWLVLCXRSNAXMCLSDFEKRRQIFAEFIYWLYNHPIIPILQSFFYITESSDLRNR
LKDFRWLFISD---TWFTKHHFENLNQLAICFISWLPRLIPKIIQTFFYCTEISSTVT-
TREISTHMQVET-SAXHFFYYFDHEN-IYVLHKLRLWIFEDLVVSLIRCFYVTEQQKSYSK
.....

Motif 1

human
ce21
EST1
p123

LFFYRKSVHSLQSIGIRQHLLXRVQLRDVSEAZVRQHRREARPAALLTSRLRFIPKP--DGL
TVYFRKDIWKLLCRPFI-TSMKMEAFEXINENNVVRMDTQK-TTLPPAVIRLLPKK--STP
TWYFRHDTWKKLITPFIYEFKTYLVENNVCRNHNHNSYTLS--RFNHSKHRIIPKKSNEEF
TYYYRKNIWDVINKHST-ADLKKETLAEVQSEKEVBEWKKK-LGFAPGKLRLLIPKK--TTF
.....

Motif 2

human
ce21
EST1
p123

RPIVNMHDYVVGARTFRREKRAERLTSRVKALP-SVLNYERA
RLITH-LRKRFLIKHGSNKKMLVSTNQTLRPVASILXHLINEESSGIPFHELVYMKLLTF
RIIAIPCRGADEEEFTIYKENHKKMAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
RPIHTFNNKIVNSDRATTKLTNTKLLNSHLHLKTLKN-RMFKDPPGPAVFNYDDVHKKY
...

Motif 3 (A)

ce21
EST1
p123

KKDLLXRMFOR-KXYFVRIDIKSCYDRIKQDLRFIVKK-KLXDPEPVIRKYATIHATS
AQRLLLKKFNNVLPELYFMKFDVKSCYDSIPRMECHRILKD-ALKNENGFFVRSQYFFSTH
EEFVCKWKQVGQPKLFFATHDIEKCYDSVNREKLSIFLKTXXLLSSDFWIMTAQILKRY
.....

Figure 2

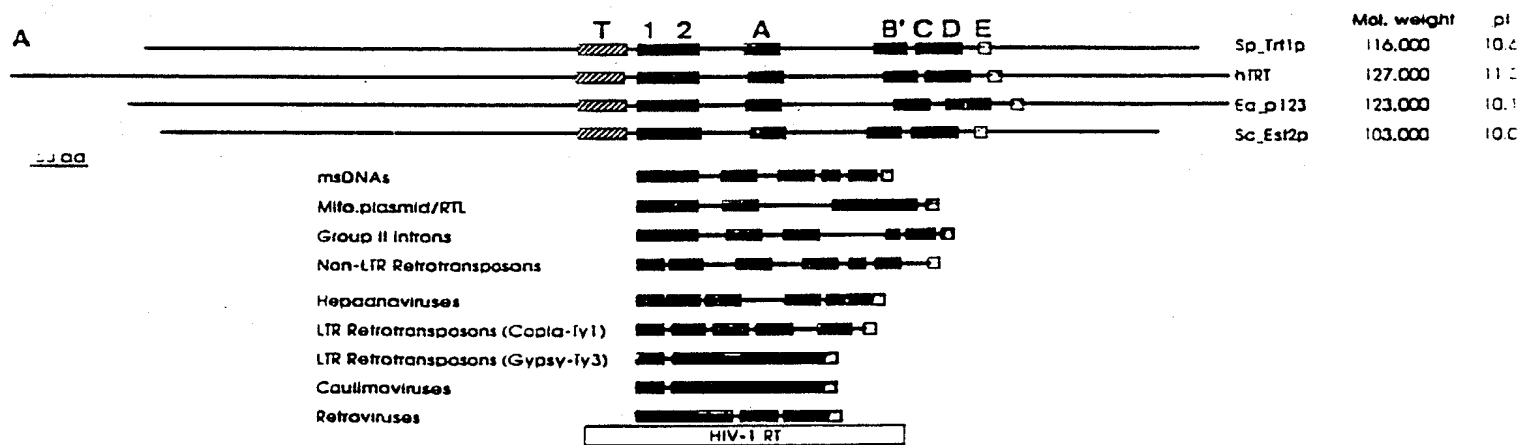


Figure 3

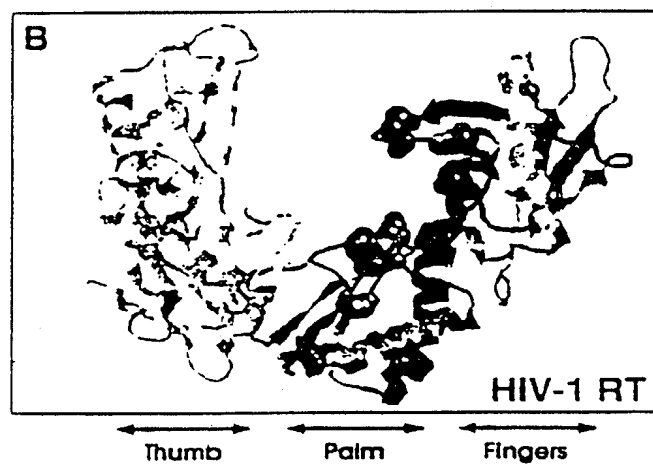


Figure 4

C									
Motif T									
TRT con	WL	hh	hh	p	Y	Y	Y	Y	K
Sp_Trtip	429	WLYNSFIIPILQST	TTTTSSDLRNR	TVYFRKDIWKLLCRPP	ITSMKM	8			
hTBT	546	WLMSSVYVVELLR	STTTTETTTFOKNRLFF	YRKSVMKLSQSIGIRQHLK	10				
Ea_p123	441	WIFEDLVVSLIRC	TTTTTEQOKSYSKTY	YKNIWDMKMSIADLKK	8				
Sc_Est2p	366	WLFRLIPKIIQT	TTTTCTEISSTVT	IVYFRHDTWNLITP	FIVEYFK	8			
Motif 1									
TRT con	h	h	h	h	h	h	h	h	h
Sp_Trtip	NNVRMDTOKTTLP	PAVIRLLPKNT	-	0	FRITNLRRFLIKMGS	NKMLVSTNOTL	40		
hTBT	EVROHREAR	PALLTSRLRFIPK	PDG	-	0	LRPIVNMDDYVGARTFR	EKRAERLTSRV	43	
Ea_p123	KEVEWKSLG	FAPCKLRLIPK	TT	-	0	FRPMTFNKKIVNSDR	KTTKLTTNTKLLN	41	
Sc_Est2p	CRNHNSYTL	SNFNHSMRIIPK	SNN	1	FRITAI	PCRGADDEEFTY	KENHKNAIOP	42	
Motif 2									
TRT con	p	h	h	h	h	h	h	h	h
Sp_Trtip	LSNELGTC	KFKPKM	RIVNIPK	PKG	0	IRPLSVGNPRDKIV	QVMMILDTIFDKK	27	
hTBT	SILRIGY	PDWAKHAQV	KMLKPGKS	6	YRPISLLSGLSK	MPERLLLR	LFRVDFK	32	
Ea_p123	EGKISKIG	PENPYNT	PVFAIRK	KDST	1	WRKLVD	PRELNKRTQDF	WEVOLGIPHPAG	0
Sc_Est2p									
Motif A									
TRT con	PcLYTh	h	h	h	h	h	h	h	h
Sp_Trtip	FGKKYF	VRIDIK	SCYDRIKODL	MFRIVEKKLKO	82				
hTBT	PPPELY	YVKVDTGAYDTI	PODRLEVIASIIKP	87					
Ea_p123	GOPKLF	FATMDIEK	CDSDVNREKLS	TFLKTTKLL	100				
Sc_Est2p	VLPELY	YMKFDVK	SCYDSIPMECH	RIKDALKN	68				
Motif B'									
TRT con	K	Y	Q	G	I	P	Q	S	L
Sp_Trtip	SOYLQKV	GIPQGS	ILSSFLCH	FYMEDLIDEYLSPT	5				
hTBT	KSYVQ	CGIPQGS	ILSTLLCS	LCYGMENKLFAGI	5				
Ea_p123	KFYKQ	TKGIPQGL	CVSSILSS	FYATLEESSLGFL	14				
Sc_Est2p	KCYIRE	DGLFQGS	SLBAPIVD	LVYDDLEFYSEFK	8				
Motif C									
TRT con	LLRL	DDFLHIT							
Sp_Trtip	LLRVVD	DFLFTVNKKD	0						
hTBT	LLRLVD	DFLLVTPHLTH	0						
Ea_p123	LMRLT	DDVLLITTOENN	0						
Sc_Est2p	ILKLAD	DFLIISTDOOQ	0						
Motif D									
TRT con	A	F	h	G	c	p	N	c	K
Sp_Trtip	AKKFLN	LSLRG	PEKHN	FSTSLERTVI	17				
hTBT	AKTFLR	TLVRG	VEYGC	VVBLRKTUV	19				
Ea_p123	AVLFIE	KLINVS	RENGFK	FMMKLOT	23				
Sc_Est2p	VINIKK	LAMGG	FOKYN	AKAMRDKILA	20				
Motif E									
TRT con	W	G	S						
Sp_Trtip	KKRM	PPFF	FFSV	181					
hTBT	HGLF	FWCG	LLLL	197					
Ea_p123	QDYC	DWIG	ISII	179					
Sc_Est2p	KELEV	WKHS	ST	146					

Figure 5

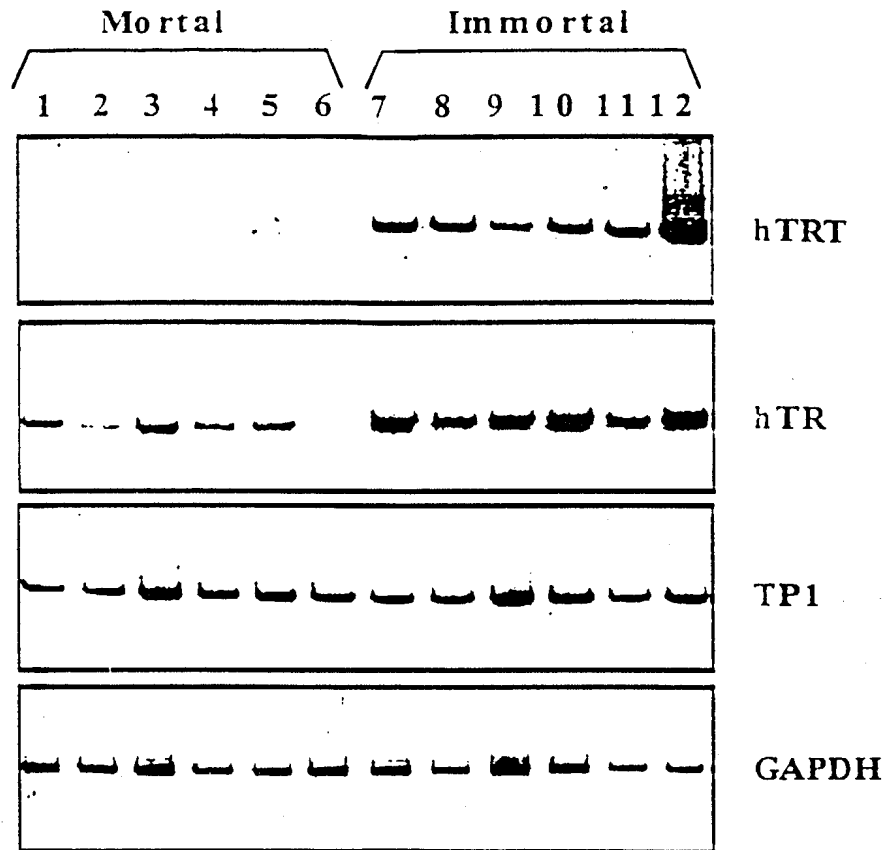


Figure 6

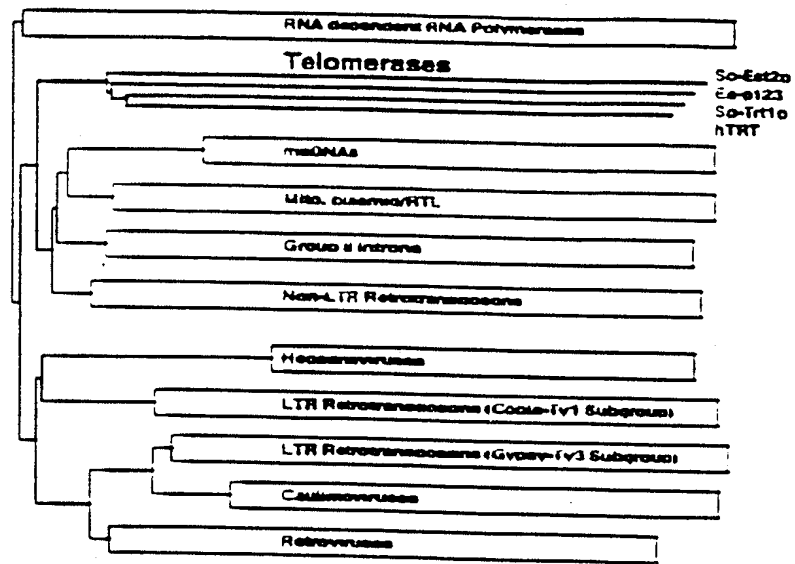


Figure 7

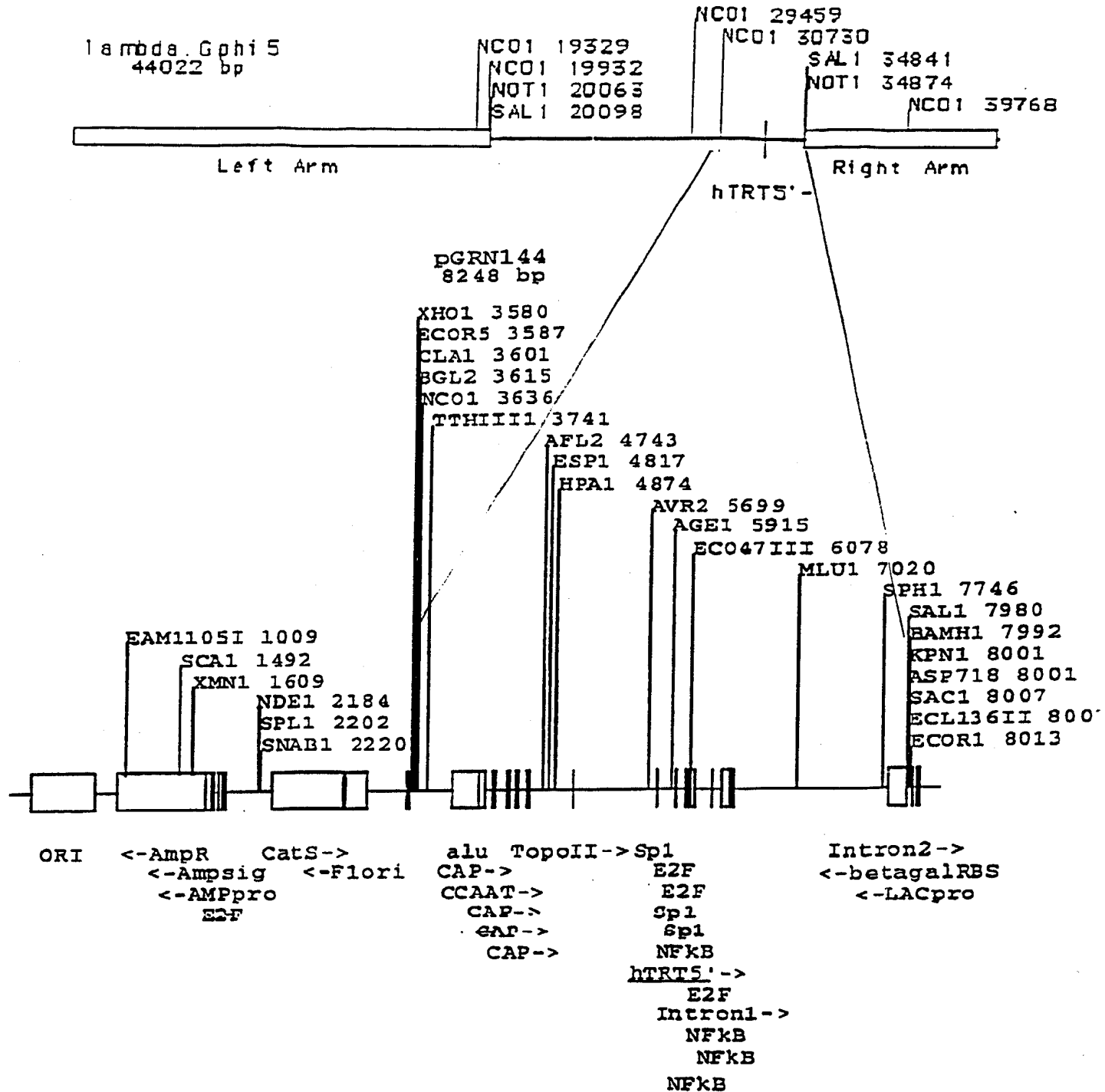


Figure 8

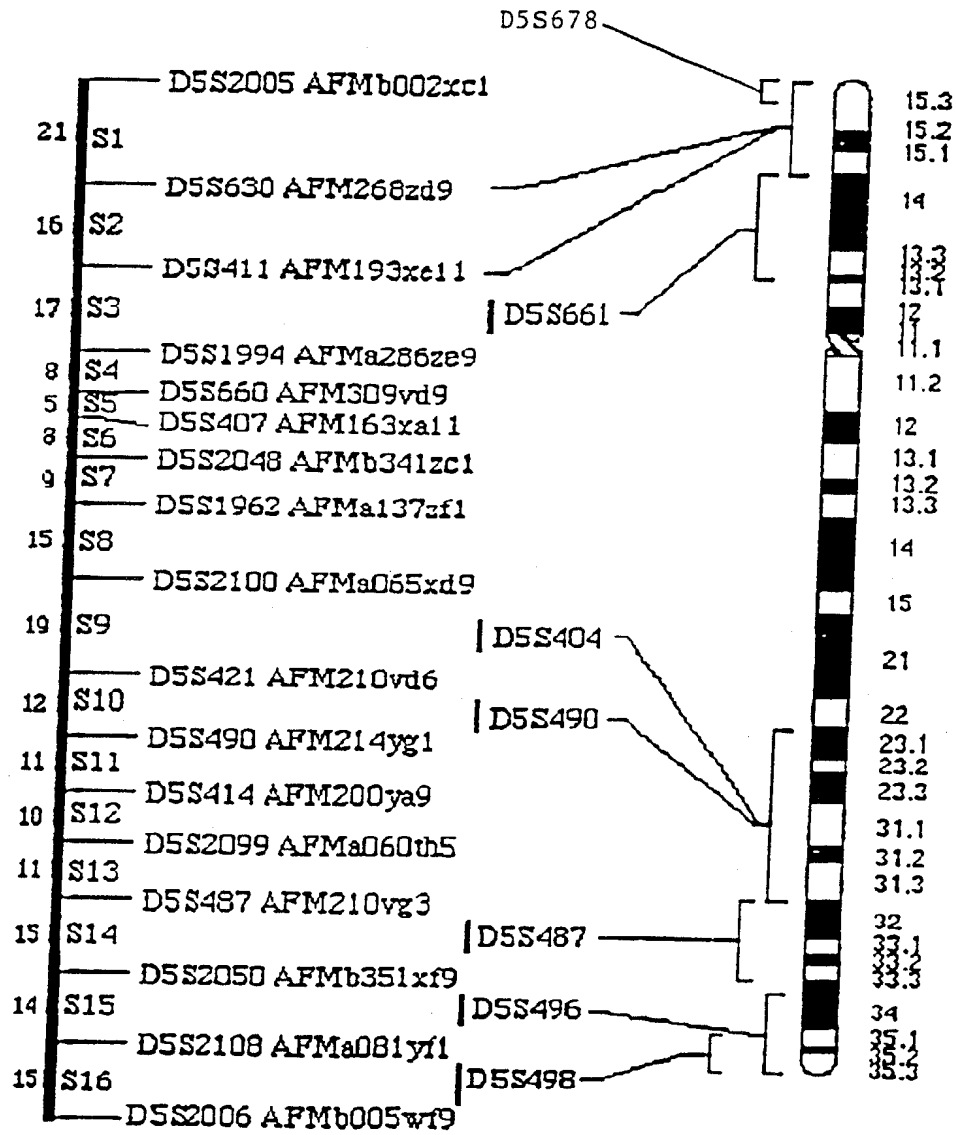
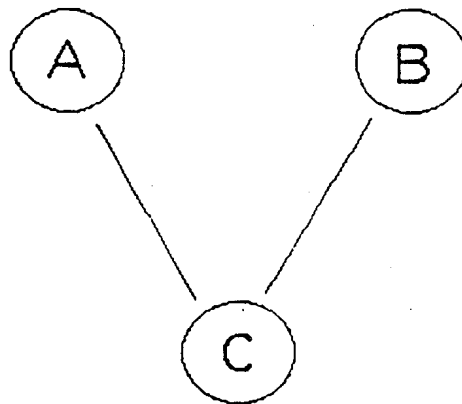
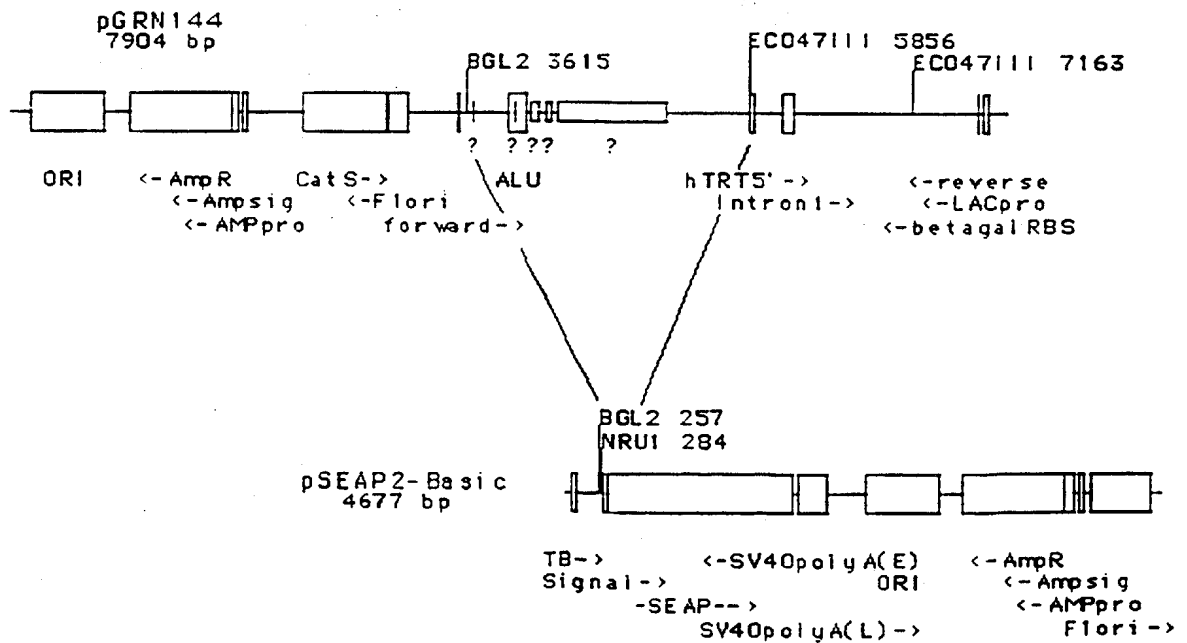


FIGURE 9

Promoter Reporter Construct



A = pGRN144
 B = pSEAP2-Basic
 C = BGL2-ECO47III fragment from A
 into BGL2-NRU1 sites of B.



Page 1



↑ PCT
↑ others

↑ other

△

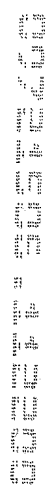


FIGURE 11

Page 1

Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	Wl	
hTRT	FFY TE	E V
spTRT	546 WLMSVYVVELLRSEFFYVTE	13 EAEVR
Ea_p123	429 WLYNSFIPIILQSFYITESSDLNRRTVYFRKDIWKLICRPFI	12 ENNVR
Sc_Est2	441 WIFEDLVSLIRCFYVTEQQKSYKTYRKNIWDVIMKMSI	12 EKEVE
	366 WLFRLIPKIIQTFYCTEISSTVT.IVYFRHDTWNKLITPFI	9 ENNVC

Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D	Y q GIPQGS lS l Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI 104 YVQCQGIPQGSILSTLLCSLCY		
spTRT	10 AVIRLLPKKNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI 99 YLQKVGIPIQGSILSSFLCHFYM		
Ea_p123	10 GKRLRLLPKKTT 0 FRPIM	67 PKLFFATMDIEKCYDSV 117 YKQTKGIPQGLCVSSILSSFFY		
Sc_Est2	13 SKMRIIPKKS 2 FRIIA	68 PELYFMKFDVKSCYDSI 85 YIREDGLFQGSLSAPIVDLVY		
RT con	p hh h K	hR h	h hDh AF h	hPQG pP hh h
				GY

FIGURE 11
Page 2

Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E	
TRT con	l l l r l D D f l i t	g n K	w g s l	
hTRT	15 L L L R L V D D F L L V T	15 G V P E Y G C V V N L R K T V V	24 W C G L L L D T R T L	192
spTRT	16 V L L R V V D D F L F I T	15 G F E K H N F S T S L E K T V I	22 F F G F S V N M R S L	176
Ea_p123	24 L L M R L T D D Y L L I T	15 V S R E N G E K F N M K K L Q T	28 W I G I S I D M K T L	174
Sc_Est2	18 L I L K L A D D F L I I S	15 G F Q K Y N A K A N R D K I L A	25 W K H S S T M N N F H	141
RT con	h Y D D h h h	G h h c k h	h L G h	
	F			

FIGURE 12

Seq. ID. No 7

181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAAGTGCCTGGTGTGCGTGCCCTGGGACGC
CCTGGGCCCGCCGAAAGGCGCGCGACCAACGGGTCACGGACCACACGCACGGGACCCTGCC

NFkB_CS1
GGGRQTYYYQC
NFkB-MHC-I.2
TGGGCTTCCCC

241 ACGGCCGCCCCCGCGCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCCGGCGTCCG
TGCCGGCGGGGGCGGCGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

Intron1

301 GCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCCACTC
CGACCCCAACTCCCGCCGGCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

NFkB_CS1
GGGRQTYYYQC
NFkB_CS2
RGGGRMTYYCC
Topo_II_cleavage_site
RNYNNCINNGYNGKTNYNY

361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCCAGTGCTGCAGAGG
TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC

Page 1 -

! AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGG
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAATAATTT TGCGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAACTTCT GAAGGAACTC TTGTTCAAT TTGCGGGAAT AACGTTTTTG
651 ATCATTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAAAT
801 ATATGAAATC AAGAACCAGA ATATTTTAAT GCACTCAAT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACCTTG
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
1151 TACACAACCTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTAC
1301 AAAAATTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAT CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAGATCC
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTT TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTAAT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAAT TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT

Figure 13

Page 2

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCCA ATAAAACCTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAAGCTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCCA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

Figure 14

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSOSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQKLG NOLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGGA
201 ADMNEPRCCS TCKYNVKNK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFRNRIRKKLK DKVIEKIAM
301 LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
401 KNLLLEKINT REISWMQVET SAKHFYFDH ENIYVLWKLL RWTFEDLVVS
451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKS LGFA PGKLR LIPKK TTFRPIMTFN KKIVNSDRKT TKLTNTKLL
551 NSHMLKTLK NRMFKDPFGF AVFNYYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
651 FRKKEMKD YF RQKFQKJALE GGQYPTLFSV LENEQN DLNA KKTLIVEAKQ
701 RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
801 INVSRENGFK FNMKKLOTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTTITE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMUD
951 LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIETSTK
1001 KYIFNRVCM I LKAKÉAKLKS DQCQSLIQYD A

Figure 15

Page 1

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1  ggtaccgattttacttttcttttcttcttaagctaatgcttctctgaacgctcctaaatctctggaaatatttttacaaga 80
81  acctataacaataaccaagtcataatctatgaaggctgtatttagtgatcgataaatatttctattttatcggtcgcta 160
161  ccaagtataaggacaaaaagaacaacttcttctctctctctctctctctctctctctctctctctctctctctctctct 240
241  ggttcgcttacttttaatcgtggtactgttttagctgctacttcttagccaacgctgtgtttcttctctctctctctct 320
321  agctctctggagtagctccacagaaatcttctctctctctctctctctctctctctctctctctctctctctctctct 400
401  ttaacatggagccttacacttttagatgagtcacgctcgcctgagtgagtgatttgggtatcatccaacgcttctgctt 480
481  gctgataactattttgcaaaatcatgctctttagtggctggttaatccgctgaaagcttttctgctgcttgcacacgctt 560
561  attgagatatttcaaaaacttctatccactacaactctctctctctctctctctctctctctctctctctctctctct 640
641  ccaaatatgtatcatctcgtattaggtcttttctctctctctctctctctctctctctctctctctctctctctct 720
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801  gatctcttgcataaacatttattagctatcatttatataaaaaaaatctctataattataaatatttaataaatattt 880
881  accttttattttaaactgttatgacagtaggacacttgcataatatatagttatgcttaactggttacttgcacttgc 958

959  ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
    1 M  T  E  H  H  T  P  K  S  R  I  L  R  F  L  E  N  Q  Y  V  20

1019  TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
    21 Y  L  C  T  L  N  D  Y  V  Q  L  V  L  R  G  S  P  A  S  S  40

1079  TAT AGC AAT ATA TCC GAA CCG TTC AGA AGC GAT GTA CAA AGC TCC TTT TCT ATT TTT CTT 1138
    41 Y  S  N  I  C  E  R  L  R  S  D  V  Q  T  S  F  S  I  F  L  60

1139  CAT TCG ACT GTA GTC CGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
    61 H  S  T  V  V  G  F  D  S  K  P  D  E  G  V  Q  F  S  S  P  80

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Page 2

[illegible]

Page 3

2337	TTC TCG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TAT ATG AGT AAC ATA AAG	2396
376	F L K L S R Y E S F S L H Y L M S N I K	395
2397	gcaatcatgccaaatttttttacccttaacttaacaacacag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA	2465
396	I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525
406	K R S N A K M C L S D F E K R K Q I F A	425
2525	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585
426	E F I Y W L Y N S F I I P I L Q S F F Y	445
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645
446	I T E S S D L R N R T V Y F R K D I W K	465
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA -ATA AAC GAG	2705
466	L L C R P F I T S M K M E A F E K I N E	485
2706	gcatttttaaagtatttttttgcaaaaaagcctaatacttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT	2775
486	N N V R M D T Q K T	495
2776	ACT TTG CCT CGA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835
496	T L P P A V I R L L P K K N T F R L I T	515
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gcatccaatttttgggtccatccaatgcaccttttacttttaactctatta	2906
516	N L R K R F L I K	524
2907	cagcgag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967
525	M G S N K K M L V S T N Q T L R P V	542
2968	GCA TCG ATA CTC AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027
543	A S I L K H L I N E E S S G I P F N L E	562
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gcaac	3088
563	V Y M K L L T F K K D L L K H R M F G	581
3089	cataataatgcgcgatcccccatcattttaatttttgtag G CGT AAG AAG TAT TTT GTA CCG ATA GAT ATA	3155
582	R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CCG ATT GTT AAA AAG AAA CTC	3215
592	K S C Y D R I K Q D L M F R I V K K K L	611
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275
612	K D P E F V I R K Y A T I H A T S D R A	631
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttttttttttcattgggaattttttaacaa	3343
632	T K N F V S E A F S Y F	643
3344	accccccttttcag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
644	D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465
660	S D T L F V D F V D Y W T X S S S E I F	679
3466	AAA ATG CTC AAG GAA CAT CTC TCT CGA CAC ATT GTT AAG gcataccaattgcctgaattgcataacaa	3532
680	K M L K E H L S G H I V K	692

Figure 15

Page 4

3533	ccaatgaaactag	ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA	3593
593		I G N S Q Y L Q K V G I P Q G S	708
3594	ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG	3653	
709	I L S S F L C H F Y M E D L I D E Y L S	728	
3654	TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA	3713	
729	F T K K K G S V L L R V V D D F L F I T	748	
3714	GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gctgagcttctgtcattccc	3777	
749	V N K K D A K K F L N L S L R G	764	
3778	caagctcttaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA	3840	
765	F E K H N F S T S L E K T V	778	
3841	ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA	3900	
779	I N F E N S N G I I N N T F F N E S K K	798	
3901	AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TCT	3960	
799	R M P F F G F S V N M R S L D T L L A C	818	
3961	CCT AAA ATT GAT GAA GGC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG	4020	
819	P K I D E A L F N S T S V E L T K H M G	838	
4021	AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagcttgacaaataaccag A TCG	4089	
839	K S F F Y K I L R	848	
4090	AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT	4149	
849	S L A S F A Q V F I D I T H N S K F N S	868	
4150	TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA	4209	
869	C C N I Y R L G Y S M C M R A Q A Y L K	888	
4210	AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gctgagctacttacttaactaga	4274	
889	R M K D I F I P Q R M F I T D	903	
4275	aaagtcatttaacttaacccag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TCG AAA AAG TTG GCC	4339	
904	L L N V I G R K I W K K L A	917	
4340	GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc	4401	
918	E I L G Y T S R R F L S S A E V K W	935	
4402	ggctctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT CGT TTC AAA	4468	
936	L F C L G M R D G L K	946	
4469	CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT	4528	
947	P S F K Y H P C F E Q L I Y Q F Q E L T	966	
4529	GAT CTT ATC AAG CCC CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA	4588	
967	D L I K P L R P V L R Q V L F L H R R I	986	
4589	GCT GAT TAA cgtcattctcttacttactatatacatcccttacttactggtgtctcttaacaatattacttacttaagcata	4665	
987	A D	989	

100% pure and free from any other substances. The purity of the product is guaranteed.

Figure 15

Page 5

4666 gctgacccccaaagcaagcataccataggaatctcttagc2aagcaaaactaactctcgttatctgctcttgattgactctgtct 4745
4746 ctatcctttatacttttaagaaagattgacagctggcttgcctgactactgccccacatgccccatc2aacgggagtggttaaaca 4825
4826 ct2aaaagtaatacatgaggttaacctctctctcatttagaataaaggaaagctggctctctataatgaataatgccccgacta 4905
4906 atgc2aaaagacgaagattatctctctaaacaagggggattcagc2atataccgaagg2aaaagagagc2aatatccccagctgtc 4985
4986 gctgaagaaagcaaggataaattctggaacaagctctctgcagatgacaggtc2aaactcttggtgacccgaactcttggt2aaaagc 5065
5066 cccaggttatccatggctggccggcctctgctactgagacg2aaaagaaactaaggatagctctgaatactaatagctcattcta 5145
5146 atgtctttatataaggtctctgctctctctgacctc2aactcttgcatgggtg2aaaagaaatagctgttaagccattattggat 5225
5226 cccgaaatagcc2aaactctctggtctctctc2aagcgggaagctct2aagaactctctg2aagctctctgaggctctc2aaaaactcc 5305
5306 tctctgattt2aaaggaggaatctctccaccgatgaggaaacgga2agcttatccagctgctgaggagaagctc2aactctctgct 5385
5386 aaaaaag2aaaatctcattgggagacatctctctgacgaac2agatg2gggagagctatctccagcggatcctctgatgctcaata 5465
5466 actctctatctctg2aacgtatggtctctaccgctcgtctc2gactctctgtagctctc2gcagctc2aagtgacc2aaaggtacc 5544

FIGURE 16
page 1
(Seq. ID. No. 1)

1 gcagcgctgc gtcctgctgc gcacgtggga agccctggcc ccggccaccc ccgcgatgcc
61 gcgcgctccc cgctgccgag ccgtgcgctc cctgctgcgc agccactacc gcgaggtgct
121 gccgctggcc acgttcgtgc ggcgcctggg gccccagggc tggcggtggg tgcagcgcg
181 ggacccggcg gctttccgcg cgctgggtgg ccagtgccctg gtgtgcgtgc cctgggacgc
241 acggccgccc ccgcgcgccc cctccttcgg ccaggtgtcc tgctgaagg agctggtggc
301 ccgagtgcctg cagaggctgt gcgagcgcg cgcgaaagac gtgctggcct tcggtctcgc
361 gctgctggac gggggccgcg gggggccccc cgaggccttc accaccagcg tgcgcagcta
421 cctgcccac acggtgaccg acgactgcg ggggagcggg gcgtgggggc tgctgctgcg
481 ccgcgtgggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt
541 ggctcccagc tgcgcctacc aggtgtgcgg gccgcgctg taccagctcg gcgctgccac
601 tcaggcccg ccgccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc
661 ctggaacat agcgtcaggg aggcgggggt cccctgggc ctgccagccc cgggtgcgag
721 gaggcgcggg ggcagtgcga gccgaagtct gccgttgccc aagaggccca ggcgtggcgc
781 tgcccctgag ccggagcgga cgcccgttgg gcaggggtcc tgggcccacc cgggcaggac
841 gcgtggaccg agtgaccgtg gtttctgtgt ggtgtcacct gccagaccgg ccgaagaagc
901 cacctctttg gagggtgcg tctctggcac gcgccactcc caccatccg tgggcccga
961 gcaccacgcg gggcccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttcc ctactcctca ggcgacaagg agcagctgcg
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggcgctcgga ggtcgtgga
1141 gaccatcttt ctgggttcca gggcctggat gccagggact cccgcaggt tgcgccgct
1201 gccccagcgc tactggcaaa tgcggccct ctgtctggag ctgcttggga accacgcga
1261 gtgcccctac ggggtgctcc tcaagacgca ctgcccgtg cgagctgcgg tcacccagc
1321 agccggtgtc tgtgcccggg agaagcccca gggctctgtg gcggcccccg agggaggga
1381 cacagacccc cgctgcctgg tgcagctgct ccgccagcac agcagccctt ggcaggtgta
1441 cggtctcgtg cgggcctgcc tgcgcgggct ggtgccccca ggctctggg gctccaggca
1501 caacgaacgc cgcttctca ggaacaccaa gaagtcatc tccctgggga agcatgccaa
1561 gctctcgtg caggagctga cgtggaagat gagcgtgcgg gactgcgctt ggctgcgcag
1621 gagcccaggg gttggctgtg ttccggccgc agagcacgt ctgctgagg agatcctggc
1681 caagtctctg cactggctga tgagtgtgta cgtcgtcgag ctgctcaggt ctttctttta
1741 tgtcacggag accacgtttc aaaagaacag gctcttttcc taccggaaga gtgtctggag
1801 caagtgtcaa agcattggaa tcagacagca cttgaagagg gtgcagctgc gggagctgtc
1861 ggaagcagag gtcaggcagc atcgggaagc caggcccgc ctgctgacgt ccagactccg
1921 cttcatcccc aagcctgacg ggctgcggcc gattgtgaac atggactacg tcgtgggagc
1981 cagaacgttc cgagagaaa agagggccga gcgtctcacc tcgagggtga aggcactgtt
2041 cagcgtgctc aactacgagc gggcgcgcg ccgcggcctc ctgggcgcct ctgtgctggg
2101 cctggacgat atccacagg cctggcgcac cttcgtgctg cgtgtgcggg cccaggaccc
2161 gccgcctgag ctgtactttg tcaagggtga tgtgacgggc gcgtacgaca ccacccccca
2221 ggacaggctc acggaggtca tcgccagcat catcaaacc cagaacacgt actgcgtgcg
2281 tcggtatgcc gtggtccaga aggcgcgcca tgggcacgtc cgcaaggcct tcaagagcca
2341 cgtctctacc ttgacagacc tccagccgta catgcgacag ttcgtggctc acctgcagga
2401 gaccagcccg ctgagggat ccgtcgtcat cgagcagagc tcctccctga atgaggccag
2461 cagtggcctc ttcgacgtct tccacgctt catgtgccac cagcgcgtgc gcacagggg
2521 caagtccctac gtcagtgcc aggggatccc gcagggtcc atcctctcca cgtgctctg
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgcg gggattcggg gggcgggct
2641 gctcctgcgt ttgggtggatg atttctgtt ggtgacacct cacctaccc acgcgaaaac
2701 cttcctcagg acctggtcc gaggtgtccc tgagtatggc tgcgtgggtga acttgcggaa
2761 gacagtgggtg aacttccctg tagaagacga ggccctgggt ggcacggctt ttgttcagat
2821 gccggcccac ggcctattcc cctgggtgcgg cctgctgctg gatacccgga ccctggaggt
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagctctc cttcaaccg

FIGURE 16
page 2
(Seq. ID. No. 1)

2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagtg
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacagggt tcacgcatgt gtgctgcagc tcccatttca
3121 tcagcaagtt tggaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctggggggcca agggcgccgc
3241 cggccctctg ccctccgagg ccgtgcagtg gctgtgccac caagcattcc tgetcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctgggggtca ctcaggacag cccagacgca
3361 gctgagtcgg aagctcccgg ggacgacgct gactgccctg gaggccgcag ccaaccgggc
3421 actgccctca gacttcaaya ccatcctgga ctgatggcca cccgccca gcccaggcca
3481 gagcagacac cagcagccct gtcacgccgg gctctacgtc ccagggaggg aggggcggcc
3541 cacacccagg cccgcaccgc tgggagtcct aggcctgagt gagtgtttgg ccgaggcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaaaggct
3661 gagtgtccag cacacctgcc gtcttcaact cccacaggc tggcgctcgg ctccaccca
3721 gggccagctt ttcctacca ggagcccgcc ttccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac ccctcgccct gccctccttt gccttccacc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtga caaagggtg
3901 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtataa tactgaatat atgagttttt cagttttgaa aaaaa

FIGURE 17
HUMAN TRT PROTEIN SEQUENCE
(SEQ. NO. 2)

MPRAPRCRAVRSLLRSHYREVLPLATFVRRLGPGWRLVQRGDP
AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRLCERGAKNVLAFGFA
LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCAFLV
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
PGARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRGPSDRGFCVVSPA
RPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPL
FLELLGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPGQSVAAPEEEDTDPRLVQ
LLROHSSPWQVYGFVRACLRLVPPGLWGSRHNERFLRNTKKFISLGKHAKLSLQEL
TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLHWLMSVYVVELLRSFFYVTET
TFQKNRLFFYRKSVWSKLQSIGIRQHLKRVQLRELSEAEVRQHREARPALLTSRLRFI
PKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKALFSVLNYERARRPGLLGASVLG
LDDIHRAWRTFVLRVRAQDPPPELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYC
VRRYAVVQKAAHGHVRKAFKSHVSTLTDLQPYMRQFVAHLOETSPLRDAVVIEQSSSL
NEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSILSTLLCSLCYGD MENKLFAG
IRRDGLLLRLVDDFLLVTPHLTHAKTFLRTLVRGVPEYGCVVNLRKTVVNFPVEDEAL
GGTAFVQMPAHGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGRNMRR
KLEGVRLRKCHSLFLDLQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQVWKNPT
FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWLCHQAFLCLKLTRHRT
YVPLLGSRLRTAQTLQSRKLPGTTLTALEAAANPALPSDFKTILD

FIGURE 18
Clone 712562
(SEQ ID NO. 3)

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
TTATGTACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG
GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCT
GTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACT
CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGCTGGG
AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT
GTTACAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGCGCCTCTGTGCT
GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGGCCAGGA
CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
CCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT
GCGTCGGTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAG
CCACGTCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT
GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCCGGCGGGACGGGC
TGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTACCCACGCGAAAA
CCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGA
AGACAGTGGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTGAGA
TGCCGGCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATAACCCGGACCCTGGAGG
TGCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACCTTCAACC
GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACCTCTTTGGGGTCTTGCGGCTGAAGT
GTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTACGCATGTGTGCTGCAGCTCCCATTTT
ATCAGCAAGTTTGAAGAACCCACATTTTTCTGCGCGTCATCTCTGACACGGCCTCCC
TCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG
CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCTGCTCAAGC
TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGC
AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAACCCGG
CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG
AGAGCAGACACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCAGGGAGGGAGGGGCGGC
CCACACCCAGGCCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGCCGAGGCCT
GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGC
TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
AGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATC
CCCAGATTGCGCATTTGTTACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC
CAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT
GCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG
GGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTG0AAAAAAAAAA
AAAAAAAAAAAAAAAAAA

FIGURE 19-

SEQ ID NO. 10

MetSerValTyrValValGluLeuLeuArgSerPhePhe
TyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerValTrp
SerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGluLeu
SerGluAlaGluValArgGlnHisArgGluAlaArgProAlaLeuLeuThrSerArgLeu
ArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValValGly
AlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAlaLeu
PheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerValLeu
GlyLeuAspAspIleHisArgAlaTrpArgThrPheValLeuArgValArgAlaGlnAsp
ProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIlePro
GlnAspArgLeuThrGluValIleAlaSerIleIleLysProGlnAsnThrTyrCysVal
ArgArgTyrAlaValValGlnLysAlaAlaHisGlyHisValArgLysAlaPheLysSer
HisValLeuArgProValProGlyAspProAlaGlyLeuHisProLeuHisAlaAlaLeu
GlnProValLeuArgArgHisGlyGluGlnAlaValCysGlyAspSerAlaGlyArgAla
AlaProAlaPheGlyGly

FIGURE 20

Page 1

SEQUENCE NO. 4 (DNA) AND SEQUENCE NO. 5 (PROTEIN) (TRANSLATION OF A $\Delta 182$ hTRT VARIANT)

```

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

50
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

80
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90

```

FIGURE 20

Page 2

130

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

140

trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

150

160

leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

170

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

180

190

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

200

leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

210

220

val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

240

250

ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

270

FIGURE 20

Page 3

280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430

FIGURE 20-

Page 4

ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440

450

ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460

leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CCG

470

480

ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490

his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500

510

leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520

met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530

540

gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550

ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560

570

leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580

arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

FIGURE 20

Page 5

590 600
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

610
 ser glu ala glu val arg gln his arg glu ala arg pro ala leu
 TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
 leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
 CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
 pro ile val asn met asp tyr val val gly ala arg thr phe arg
 CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650 660
 arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
 AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
 phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
 CTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680 690
 gly ala ser val leu gly leu asp asp ile his arg ala trp arg
 GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
 thr phe val leu arg val arg ala gln asp pro pro pro glu leu
 ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710 720
 tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
 TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
 gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
 CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

FIGURE 20

Page 6

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

760
his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

770 780
val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

790
gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

800 807
ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTGTTGGT

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA
GTATGGCTGCGTGGTGAACCTTGCGGAAGACAGTGGTGAACCTTCCTGTAGAAGACGAGGC
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCACGGCCTATTCCCCTGGTGCGGCCT
GCTGCTGGATAACCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA
ACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAG
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGAAGAACCCACATTTTTCCT
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG
GATGTCGCTGGGGGCCAAGGGCGCCGCCGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCT
GTGCCACCAAGCATTTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCT

FIGURE 20

Page 7

GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC
TGCCCTGGAGGCCGCGAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG
ATGGCCACCCGCCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTCACGCCGGGCT
CTACGTCCCAGGGAGGGAGGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG
GCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC
CACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTC
CACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTACCCCCTCGCCCTGCC
CTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC
TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT
GGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG
AGTTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 21 -
Genomic DNA insert of pGRN144

Seq. ID. No. 6

```
1  CCATGGGACCCACTGCAGGGGCAGCTGGGAGGCTGCAGGCTTCAGGTCCCAGTGGGGTTG
   GGTACCCTGGGTGACGTCCCCGTCGACCCTCCGACGTCCGAAGTCCAGGGTCACCCCAAC

61  CCATCTGCCAGTAGAAACCTGATGTAGAATCAGGGCGCGAGTGTGGACACTGTCCTGAAT
   GGTAGACGGTCATCTTTGGACTACATCTTAGTCCCGCGCTCACACCTGTGACAGGACTTA

121 CTCAATGTCTCAGTGTGTGCTGAAACATGTAGAAATTAAAGTCCATCCCTCCTACTCTAC
   GAGTTACAGAGTCACACACGACTTTGTACATCTTTAATTTTCAGGTAGGGAGGATGAGATG

181 TGGGATTGAGCCCCCTTCCCTATCCCCCCCCAGGGGCAGAGGAGTTCCTCTCACTCCTGTG
   ACCCTAACTCGGGGAAGGGATAGGGGGGGGTCCCCGTCTCCTCAAGGAGAGTGAGGACAC

241 GAGGAAGGAATGATACTTTGTTATTTTTCAGTGTGGTACTGAATCCACTGTTTCATTTG
   CTCCTTCCTTACTATGAAACAATAAAAAGTGACGACCATGACTTAGGTGACAAAGTAAAC

   *****

301 TTGGTTTGTTTGTTTGTGTTTGGAGAGGCGGTTTCACTCTTGTTGCTCAGGCTGGAGGGAG
   AACCAAACAAACAAACAAAACTCTCCGCCAAAGTGAGAACAACGAGTCCGACCTCCCTC

   *****

361 TGCAATGGCGCGATCTTGGCTTACTGCAGCCTCTGCCTCCCAGGTTCAAGTGATTCTCCT
   ACGTTACCGCGCTAGAACCGAATGACGTCGGAGACGGAGGGTCCAAGTTCACCTAAGAGGA

   alu
   *****

421 GCTTCCGCCTCCCATTTGGCTGGGATTACAGGCACCCGCCACCATGCCAGCTAATTTTTT
   CGAAGGCGGAGGGTAAACCGACCCTAATGTCCGTGGGCGGTGGTACGGGTGATTAAAAA

   ==

   *****

481 TGTATTTTTAGTAGAGACGGGGGTGGGGGTGGGGTTCACCATGTTGGCCAGGCTGGTCTC
   ACATAAAAATCATCTCTGCCCCACCCCCACCCCAAGTGGTACAACCGGTCCGACCAGAG

   CAP
   =====>

   *****

1 541 GAACTTCTGACCTCAGATGATCCACCTGCCTCTGCCTCCTAAAGTGCTGGGATTACAGGT
   CTTGAAGACTGGAGTCTACTAGGTGGACGGAGACGGAGGATTTACGACCCTAATGTCCA

   *****

601 GTGAGCCACCATGCCAGCTCAGAATTTACTCTGTTTAGAAACATCTGGGTCTGAGGTAG
   CACTCGGTGGTACGGGTGAGTCTTAAATGAGACAAATCTTTGTAGACCCAGACTCCATC
```

FIGURE 21 (continued, 2 of 6)

CCAAT

*****>

661 GAAGCTCACCCCACTCAAGTGTGTGGTGTTTTAAGCCAATGATAGAATTTTTTTATTGT
CTTCGAGTGGGGTGAGTTCACAACACCACAAAATTCGGTTACTATCTTAAAAAATAACA

721 TGTTAGAACACTCTTGATGTTTTTACACTGTGATGACTAAGACATCATCAGCTTTTCAAAG
ACAATCTTGTGAGAACTACAAAATGTGACACTACTGATTCTGTAGTAGTCGAAAAGTTTC

CAP

*****>

781 ACACACTAACTGCACCCATAATACTGGGGTGTCTTCTGGGTATCAGCGATCTTCATTGAA
TGTGTGATTGACGTGGGTATTATGACCCACAGAAGACCCATAGTCGCTAGAAGTAACTT

CAP

841 TGCCGGGAGGCGTTTCCTCGCCATGCACATGGTGTAAATTACTCCAGCATAATCTTCTGC
ACGGCCCTCCGCAAAGGAGCGGTACGTGTACCACAATTAATGAGGTCTGATTAGAAGACG

***>

901 TTCCATTTCTTCTCTTCCCTCTTTTAAAATTGTGTTTTCTATGTTGGCTTCTCTGCAGAG
AAGGTAAAGAAGAGAAGGGAGAAAATTTTAACACAAAAGATACAACCGAAGAGACGTCTC

CAP

*****>

961 AACCAGTGTAAGCTACAACCTAACTTTTGTGGAAACAAATTTTCCAAACCGCCCTTTGC
TTGGTTCACATTCGATGTTGAATTGAAAACAACCTTGTTTAAAAGGTTTGGCGGGGAAACG

1021 CCTAGTGGCAGAGACAATTCACAAACACAGCCCTTTAAAAGGCTTAGGGATCACTAAGG
GGATCACCGTCTCTGTTAAGTGTGTTGTGTCGGGAAATTTTCCGAATCCCTAGTGATTCC

1081 GGATTTCTAGAAGAGCGACCCGTAATCCTTAAGTATTTACAAGACGAGGCTAACCTCCAG
CCTAAAGATCTTCTCGCTGGGCATTAGGAATTCATAAATGTTCTGCTCCGATTGGAGGTC

1141 CGAGCGTGACAGCCCAGGGAGGGTGCGAGGCCTGTTCAAATGCTAAGCTTCATAAATAA
GCTCGCACTGTCCGGTCCCTCCACGCTCCGGACAAGTTTACGATTCCAAGGTATTTATT

1201 AGCAAATTTCTCCGGCAGTTTCTGGAAAGTAGGAAAGGTTAACATTTAAGGTTGCGTTT
TCGTTTAAAGGAGGCCGTCAAAGACCTTTCATCCTTTCCAATTGTAAATTTCAACGCAAA

1261 GTTAGCATTTTCAGTGTTTGCCGACCTCAGCTAACAGCATCCCTGCAAGGCCTCGGGAGAC
CAATCGTAAAGTCACAAACGGCTGGAGTCGATTGTCTGCTAGGGACGTTCCGGAGCCCTCTG

1321 CCAGAAAGTTTCTCGCCCTTAGATCCAACTTGAGCAACCCGGAGTCTGGATTCTCGGGA
GGTCTTCAAAGAGCGGGGAATCTAGGTTTGAACCTCGTTGGGCCTCAGACCTAAGGACCCT

TopoII

*****>

1381 AGTCCTCAGCTGTCTGCGGTTGTGCCGGGGCCCCAGGTCTGGAGGGGACCAGTGCCGT
TCAGGAGTCGACAGGACGCCAACACGGCCCCGGGGTCCAGACCTCCCCTGGTCACCGGCA

1441 GTGGCTTCTACTGCTGGGCTGGAAGTCGGGCCTCCTAGCTCTGCAGTCCGAGGCTTGGAG
CACCGAAGATGACGACCCGACCTTCAGCCCGGAGGATCGAGACGTCAGGCTCCGAACCTC

FIGURE 21 (continued, 3 of 6)

1501 CCAGGTGCCTGGACCCCGAGGCTGCCCTCCACCCTGTGCGGGCGGGATGTGACCAGATGT
GGTCCACGGACCTGGGGCTCCGACGGGAGGTGGGACACGCCCGCCCTACACTGGTCTACA

1561 TGGCCTCATCTGCCAGACAGAGTGCCGGGGCCAGGGTCAAGGCCGTTGTGGCTGGTGTG
ACCGGAGTAGACGGTCTGTCTCACGGCCCCGGGTCCCAGTTCGGCAACACCGACCACAC

1621 AGGCGCCCGGTGCGCGGCCAGCAGGAGCGCCTGGCTCCATTCCCACCCTTTCTCGACGG
TCCGCGGGCCACGCGCCGGTCTGTCTCGCGGACCGAGGTAAAGGGTGGGAAAGAGCTGCC

1681 GACCGCCCCGGTGGGTGATTAACAGATATTGGGGTGGTTTGCTCATGGTGGGGACCCCTT
CTGGCGGGGCCACCCACTAATTGTCTATAACCCACCAAACGAGTACCACCCTGGGGAA

1741 CGCCGCCTGAGAACCTGCAAAGAGAAATGACGGGCCTGTGTCAAGGAGCCCAAGTCGCGG
GCGGCGGACTCTTGGACGTTTCTCTTTACTGCCCGGACACAGTTCCTCGGGTTCAGCGCC

1801 GGAAGTGTGTCAGGGAGGCACTCCGGGAGGTCCCGCGTGCCCGTCCAGGGAGCAATGCGT
CCTTCACAACGTCCCTCCGTGAGGCCCTCCAGGGCGCACGGGCAGGTCCCTCGTTACGCA

1861 CCTCGGGTTCGTCCCCAGCCGCGTCTACGCGCCTCCGTCTCCCTTCACGTCCGGCATT
GGAGCCCAAGCAGGGGTCTGGCGCAGATGCGCGGAGGCAGGAGGGGAAGTGCAGGCCGTAA

1921 CGTGGTGCCCGGAGCCCGACGCCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGA
GCACCACGGGCCTCGGGCTCGGGGGCGCAGGCCTGGACCTCCGTCTGGGACCCAGAGGCCT

1981 TCAGGCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCCAGGGCCTCCACATCATGGC
AGTCCGGTCTCGCCGTTTCCCAGCGCGTTCGTGGACAAGGGTCCCAGGAGGTGTAGTACCG

2041 CCCTCCCTCGGGTTACCCACAGCCTAGGCCGATTTCGACCTCTCTCCGCTGGGGCCCTCG
GGGAGGGAGCCCAATGGGGTGTCTGGATCCGGCTAAGCTGGAGAGAGGCGACCCCGGGAGC

Sp1

2101 CTGGCGTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCAGAC
GACCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCTTCGCGCCGGGTCTG

2161 CCCCGGGTCCGCCCCGAGCAGCTGCGCTGTGCGGGCCAGGCCGGGCTCCAGTGGATTCTG
GGGGCCCAGGCGGGCCTCGTCGACGCGACAGCCCCGGTCCGGCCCCAGGGTCACTAAGC

2221 CGGGCAACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAGGGACTGGGGACCCGGGCA
GCCCGTTGTCTGCGGGTCTGGCGGAAGGGTGACCGCCTCCCTGACCCCTGGGCCCGT

Sp1

=====

E2F

2281 CCGGTCCTGCCCCCTTACCTTCCAGCTCCGCCCTCGTCCGCGCGGAACCCCGCCCCGTCCC
GGCCAGGACGGGGAAGTGGAAGGTGAGGCGGAGCAGGCGCGCCTTGGGGCGGGGCAGGG

2341 GAACCCTTCCCGGGTCCCCGGCCCCAGCCCCCTTCCGGGCCATCCAGCCCCGTCCCGTTCTT
CTTGGGAAGGGCCCAGGGGCCGGGTCTGGGAAGGCCCGGTAGGGTGGGCAGGGCAAGGA

FIGURE 21 (continued, 4 of 6)

```

                Sp1
            =====

            E2F
            *****
2401 TTTCCGCGGCCCCCGCCCTCTCCTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCTGC
    AAAGGCGCCGGGGCGGGAGAGGAGCGCCGCGCTCAAAGTCCGTGCGGACGACGAGGACGACG

            hTRT5'
            *****>
2461 GCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCGATGCCGCGCGCTCCCCGCTGCCGAG
    CGTGACCCCTTCGGGACCGGGGCGGTTGGGGGCGCTACGGCGCGCGAGGGGGCGACGGCTC

2521 CCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGC
    GGCACGCGAGGGACGACGCGTCGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCAGC

                                                    E2F
                                                    *****
2581 GCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGGCTTTCCGCG
    CCGCGGACCCCGGGTCCCGACCGCCGACCACGTCGCGCCCCCTGGGCGCGCGAAAGGCGC

    *
2641 CGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGCGCC
    GCGACCACCGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGGCGGCGGG

                NFkB
            =====

            *****
2701 CCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCCGCGTCCGGCTGGGGTTGAGGGCGGCGC
    GGAGGAAGGCGGTCCACCCGAGGGGGCCCCAGCCGACGGCCGACCCCAACTCCCGCCGGC

                                                    Topo_II_cleavag
                                                    ::::::::::::::
                                                    NFkB
                                                    ++++++++++
                                                    NFkB
                                                    =====

            Intron1
            *****>
2761 GGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGT
    CCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCA

            e_site
            ::::

2821 GTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAA
    CAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTT

2881 GAACGTGCTGGCCTTCGGCTTCGCGTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGC
    CTTGCACGACCGGAAGCCGAAGCGCGACGACCTGCCCGGGGCGCCCCCGGGGGGGCTCCG

2941 CTTACCAACAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAG
    GAAGTGGTGGTCGACGCGTCGATGGACGGGTTGTGCCACTGGCTGCGTGACGCCCCCTC

```

FIGURE 21 (continued, 5 of 6)

3001 CGGGGCGTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGC
GCCCCGACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCG

3061 ACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCC
TGCGACGCGCGAGAAACACGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCCGGCGG

3121 GCTGTACCAGCTCGGCGCTGCCACTCAGGCCCCGGCCCCCGCCACACGCTAGTGGACCCCG
CGACATGGTTCGAGCCGCGACGGTGAGTCCGGGCGGGGGCGGTGTGCGATCACCTGGGGC

3181 AAGGCGTCTGGGATGCGAACGGGCCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCT
TTCCGACAGACCCTACGCTTGCCCGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGA

3241 GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT
CCCGGACGGTCGGGGCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAA

3301 GCCCAAGAGGCCCCAGGCGTGCGCTGCCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGG
CGGGTTCTCCGGGTCCGCACCCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTC

3361 GTCCTGGGCCCCACCCGGGCGAGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTC
CAGGACCCGGGTGGGCCCCGTCTGCGCACCTGGCTCACTGGCACCAAGACACACCACAG

3421 ACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCA
TGGACGGTCTGGGCGGCTTCTTCGGTGGAGAACTCCACGCGAGAGACCGTGCGCGGT

3481 CTCCCACCCATCCGTGGGCGGCCAGCACCCACGCGGGCCCCCATCCACATCGCGGCCACC
GAGGGTGGGTAGGCACCCGGCGGTCTGTGGTGCGCCCCGGGGGTAGGTGTAGCGCCGGTGG

3541 ACGTCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTC
TGCAGGGACCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCTGTGAAGGAGATGAG

3601 CTCAGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCAGCCT
GAGTCCGCTGTTCTCTGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTGCGA

3661 GACTGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG
CTGACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCC

3721 GACTCCCCGCGAGGTTGCCCCGCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCT
CTGAGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGA

3781 GGAGCTGCTTGGGAACCACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCC
CCTCGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGG

3841 GCTGCGAGCTGCGGTACCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCAGGGCTC
CGACGCTCGACGCCAGTGGGGTCGTGCGCCACAGACACGGGCCCTCTTCGGGGTCCCGAG

3901 TGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCGTCGCTGGTGCAGCTGCTCCGCCA
ACACCGCCGGGGGCTCCTCCTCTGTGTCTGGGGGCAGCGGACCACGTCGACGAGGCGGT

3961 GCACAGCAGCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCC
CGTGTCGTGCGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACCACGG

4021 CCCAGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTT
GGGTCCGGAGACCCCGAGGTCCGTGTTGCTTGCGGCGAAGGAGTCCTTGTGGTTCTTCAA

FIGURE 21 (continued, 6 of 6)

4081 CATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGT
GTAGAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCCTCGACTGCACCTTCTACTCGCA

4141 GCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTCGAGGGCCC
CGCCCTGACGCGAACCACGCGTCCTCGGGTCCACTCCTCCACCACCGGCAGTCCCGGG

Intron2

4201 AGGCCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCT
TCCGGGGTCTCGACTTACGTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGA

4261 CCTGTCTCCATCGTACGTGGGCACACGTGGCTTTTCGCTCAGGACGTCGAGTGGACACG
GGACAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCCTGCAGCTCACCTGTGC

*****>

4321 GTGATCGAGGTTCGAC
CACTAGCTCCAGCTG

Figure 22

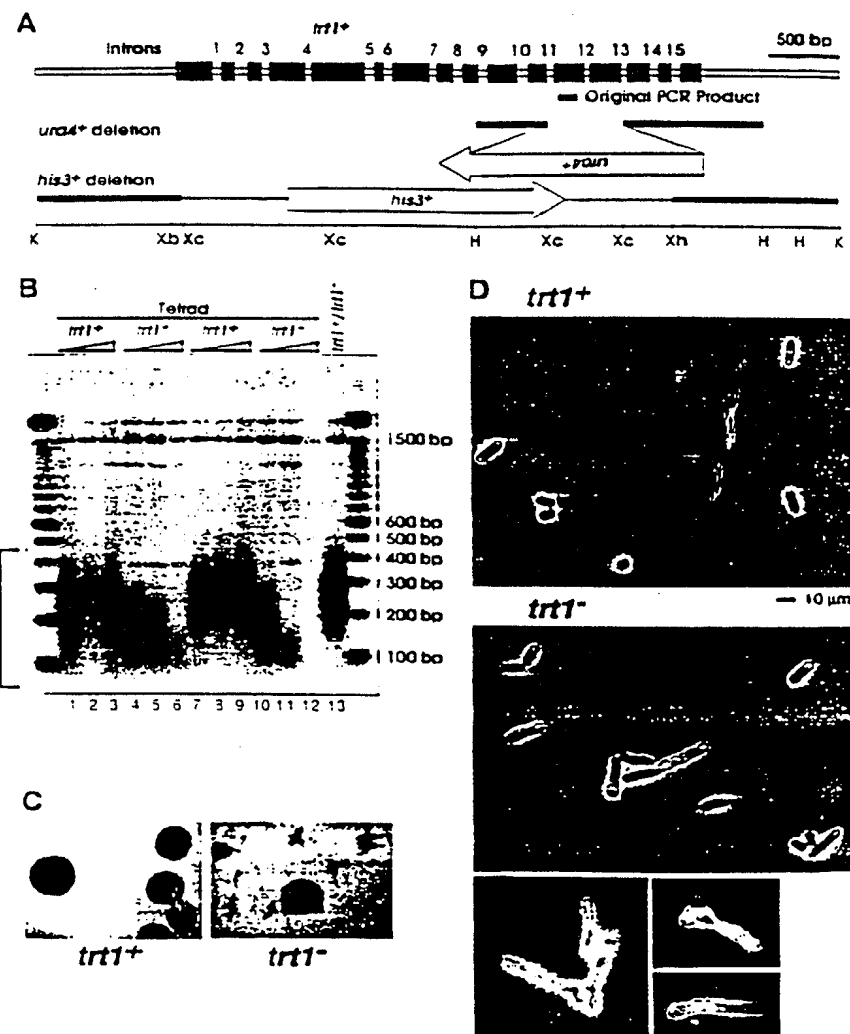


FIGURE 23
EST AA281296
(Seq. ID. No. 8)

gc

caagttcctg	cactgggtga	tgagtgtgta	cgtcgtcgag	ctgctcaggt	ctttctttta
tgtcacggag	accacgtttc	aaaagaacag	gctctttttc	taccggaaga	gtgtctggag
caagttgcaa	agcattggaa	tcagacagca	cttgaagagg	gtgcagctgc	gggacgtgtc
ggaagcagag	gtcaggcagc	atcggaagc	caggcccgcc	ctgctgacgt	ccagactccg
cttcattccc	aagcctgacg	ggctgcgggc	gattgtgaac	atggactacg	tcgtgggagc
cagaacgttc	cgcagagaaa	agagggccga	gcgtctcacc	tcgaggggtga	aggcactggt
cagcgtgctc	aactacgagc	gggcgcgc			

11

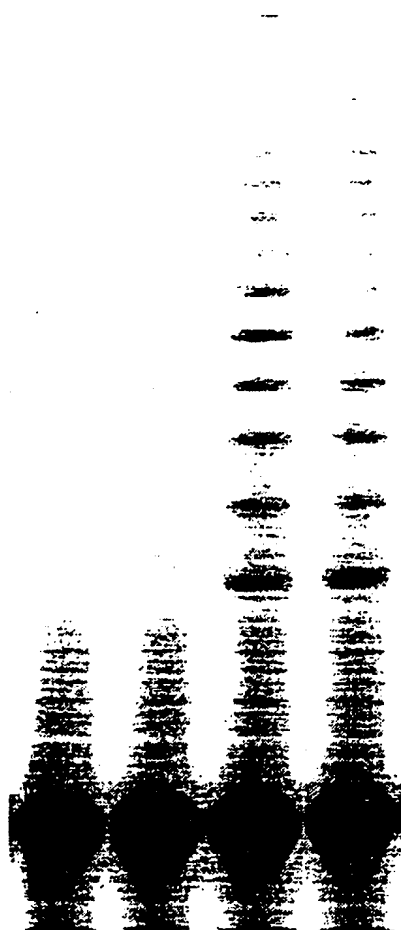
FIGURE 24 -
(Seq. ID. No. 9)

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
ACCAGCCCCGCTGAGGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGC
CAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCAT
CAGGGGCAAGTC

Figure 25

pBB5212

pGRN133



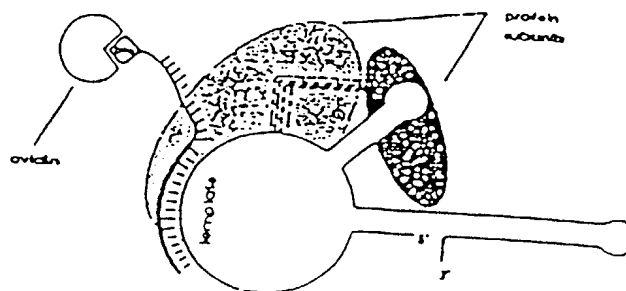
← Internal Control

Approximate Cell No.

5,000 5,000 5,000 5,000

Figure 26

PANEL A



PANEL B

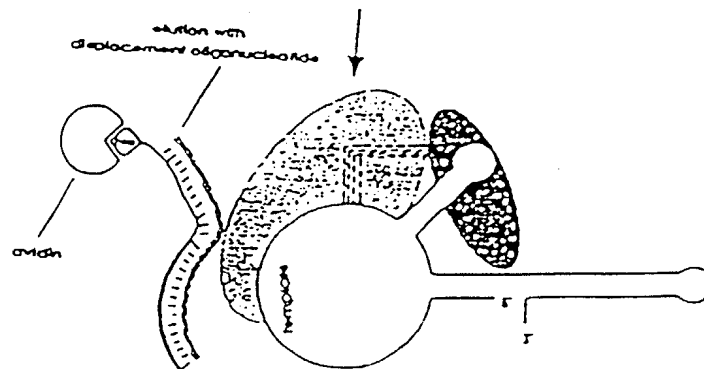


Figure 27

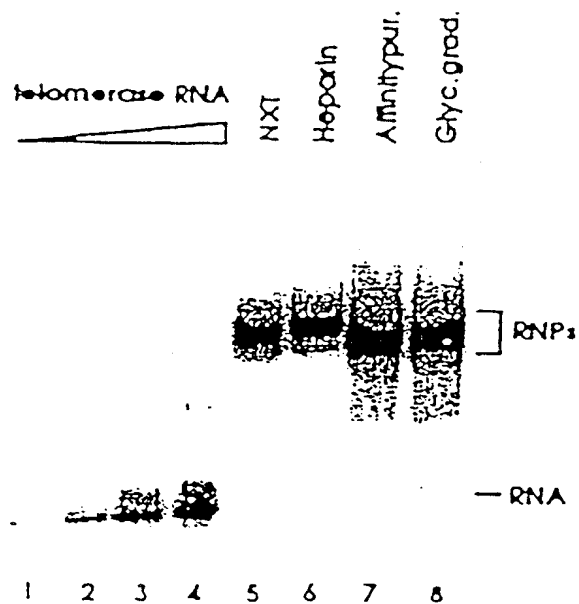


Figure 28

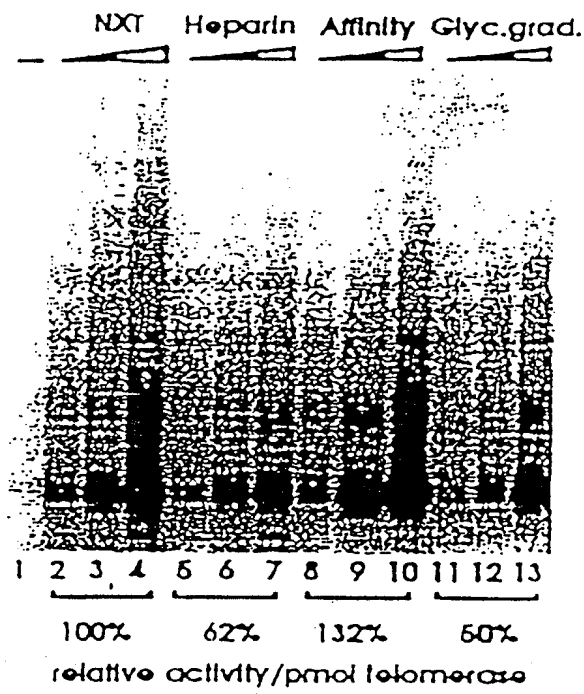


Figure 29

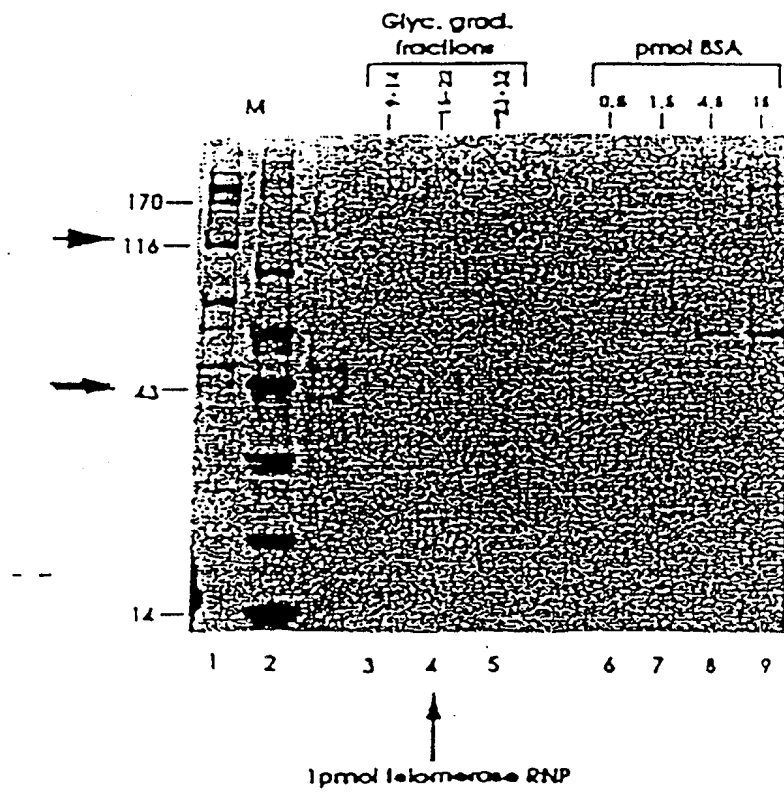


Figure 30

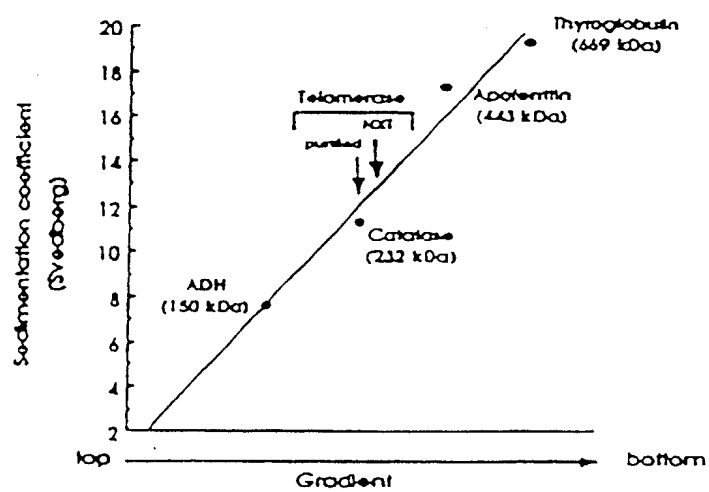


Figure 31 -

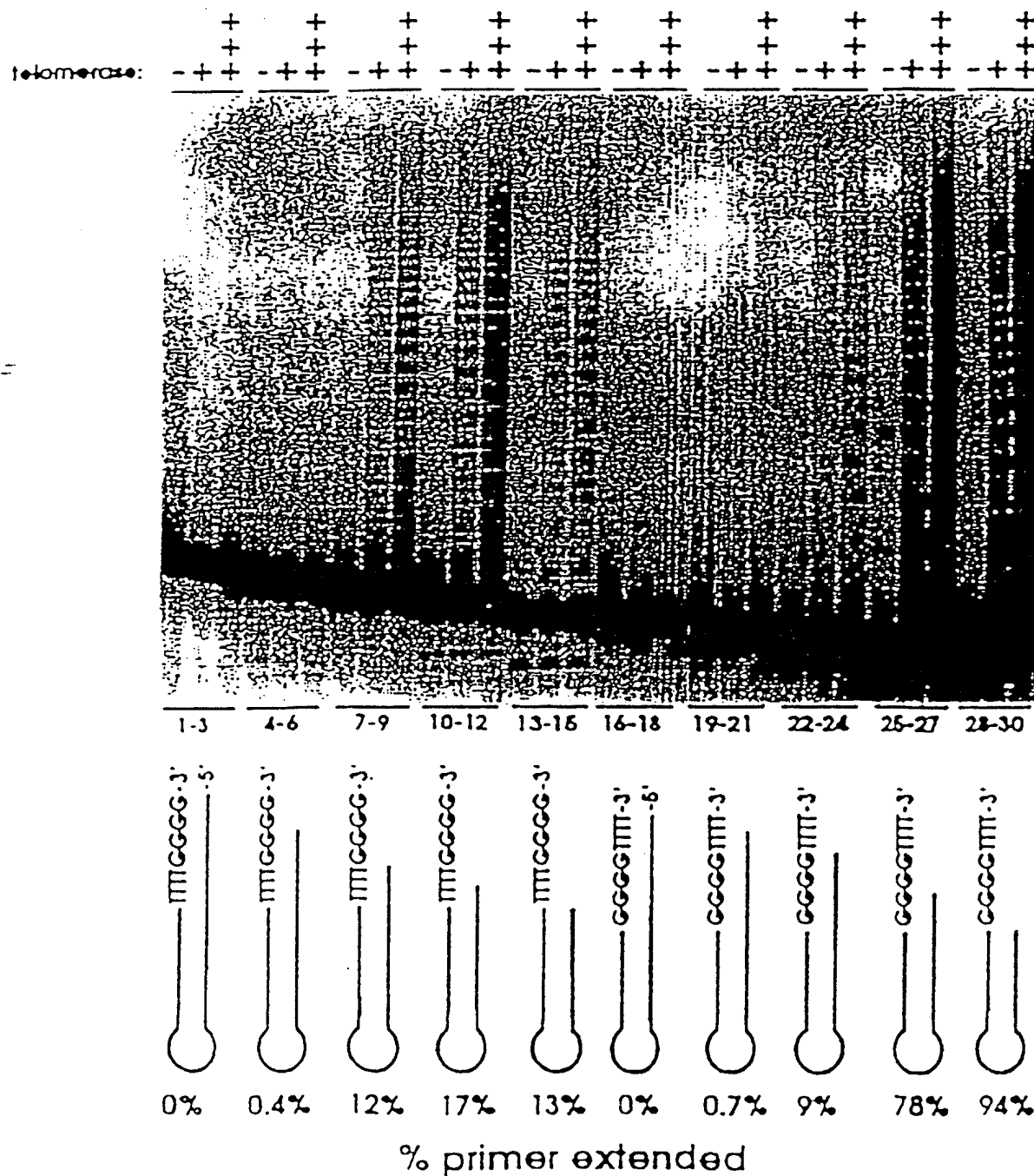


Figure 32

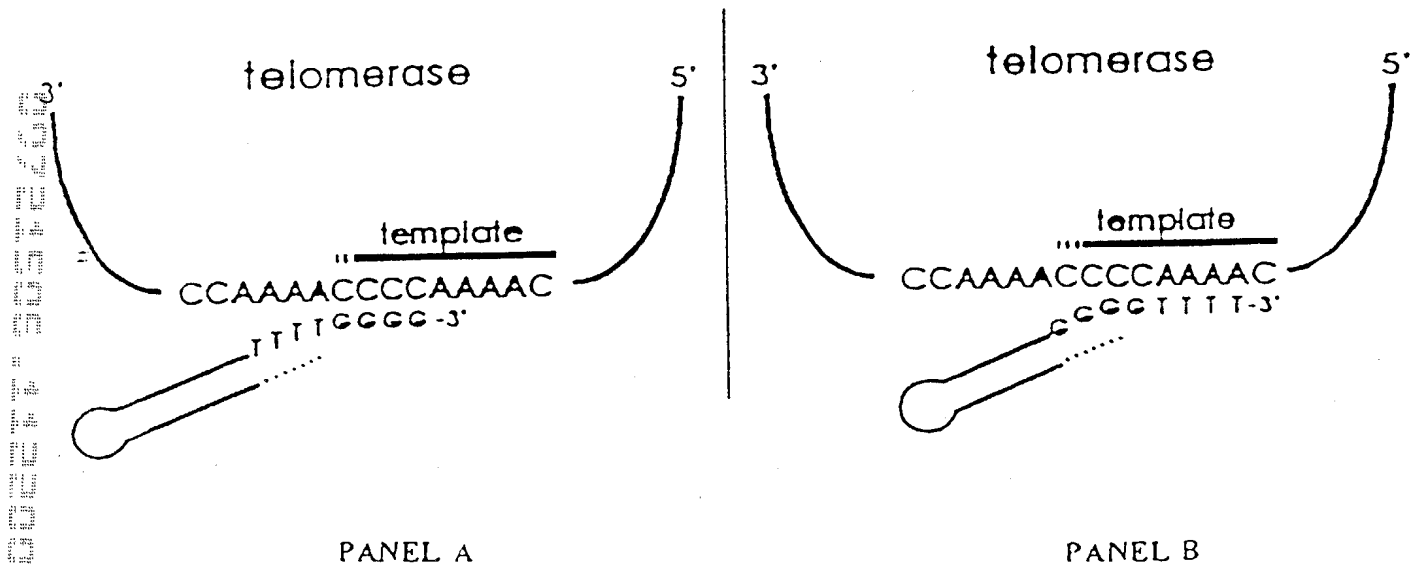


Figure 33



Figure 34

1 CCCCAAAACC CCAAACCCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
51 GTAGTTTGA AATAAAATAT TATTCCTGCA CAAATGGAGA TGGATATTGA
101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCT
601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
651 TTGAGACAAT TGAAAAAGCT GTTTACAACCT GAAGGAATCG CAGTTCTGAA
701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
801 TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
951 AAAAGAAGCA GCGGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001 TTGTTGATTG TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051 AAAGAAGAAG AGCTATCACA ATCCTGATTG TTAAGATTG CAAAAATTCC
1101 AGGTAAGAGA GATACATTCA TTAAGATTG TATATTATAG TTTTCAATT
1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA
1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751 GGGGTTTTGG GG

1 CCCC AAAACCCCAA AAAACCCCAA ACCCTATAAAAAAGAAAAATTGAGGTAGTTTAGA
 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
 GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTTCTTTTTTAACCTCATCAAATCT

 a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N * G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -

 AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
 61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
 TTATTTTATAATAAGGGCGTGTTTACCTCTACCTATAACTAAACCTACTATATCTTTTAA

 a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y * F G * Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -

 TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTTCTACGTTTT

 a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * C Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -

 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
 GTAACCTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

 a H * N L A R N R L H * L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -

 AGTTCTACTTCTCGGATGCAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
 TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

 a S S T S R M Q I F I T I L S * E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

 AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
 TTTGCGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

 a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N * N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -

 TGAGGATTATTCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

 a * G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 35

421 TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
 ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

 a Y * K V N S L D Y F P S Q Q * * V Y * I -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T M M S I L N S -

 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
 481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
 GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

 a H M R M S Q R I S I H Q T Y Q R Q T R Y -
 b I * E * V K G S R Y I R L T K D K L A I -
 c Y E N E S K D L D T S D L P K T N S L * -

 AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCTG
 541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
 TTTTGCGTTCTTTTCAAACCTATTAGCTTGTCTCTTCTTGAATAACGTAAATGATAAGC

 a K T Q E K V * * S N S R R T Y C I Y Y S -
 b K R K K K F D N R T A E E L I A F T I R -
 c N A R K S L I I E Q Q K N L L H L L F V -

 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCCGAGTCTTGAGACAAT
 601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
 ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

 a Y G F Y Y N C F R Y R R * T P E S * D N -
 b M G F I T I V L G I D G E L P S L E T I -
 c W V L L Q L F * V S T V N S R V L R Q L -

 TGAAAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
 ACTTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

 a * K S C L Q L K E S Q F * K F C C V C H -
 b E K A V Y N * R N R S S E S S D V Y A I -
 c K K L F T T E G I A V L K V L M C M P L -

 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
 ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

 a Y F V N * S Q I S Y L N L M D S Y R N K -
 b I L * I N L K Y L I S I * W I A I E T N -
 c F C E L I S N I L S Q F N G * L * K Q T -

 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
 781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

 a P N K P C K F N G I Y V K S F G T N A H -
 b Q I N H A S L M E Y T L N P L G Q M H T -
 c K * T M Q V * W N I R * I L W D K C T L -

 TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
 841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 ACTTAAATATAACCTAAGAATTTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

 a * I Y I G F L K H R Y T E C F R D * F S -
 b E F I L D S * S I D T Q N A L E T D L A -
 c N L Y W I L K A * I H R M L * R L I * L -

FIG. 35
 (CONTINUED)

TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
 901 -----+-----+-----+-----+-----+ 960
 AATGTTGTCTAATGGACAAAATAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

 a L Q Q I T C F D Y S C S S L I S L K E A -
 b Y N R L P V L I T L A H L L Y L * K K Q -
 c T T D Y L F * L L L L I S Y I F K R S R -

 GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 -----+-----+-----+-----+-----+ 1020
 CCGCTTTACTTTTCTCTGATTCTTCTCTCTAAAGTTTAAACAACCTAAGAAGACATTGG

 a G E M K R R L K K E I S K F V D S S V T -
 b A K * K E D * R K R F Q N L L I L L * P -
 c R N E K K T K E R D F K I C * F F C N R -

 GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC
 1021 -----+-----+-----+-----+-----+ 1080
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTCTCTCTCGATAGTGTAGGACTAAG

 a G I N N K N I S N E K K E E L S Q S * F -
 b E L T T R I L A T K K K S Y H N P D S -
 c N * Q Q E Y * Q R K R R R A I T I L I L -

 TTAAAGATTTCAAAATTCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
 1081 -----+-----+-----+-----+-----+ 1140
 AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAACTATATAATATC

 a L K I S K I P G K R D T F I K I H I L * -
 b * R F Q K F Q V R E I H S L K F I Y Y S -
 c K D F K N S R * E R Y I H * N S Y I I V -

 TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTGATTAGCTGGAA
 1141 -----+-----+-----+-----+-----+ 1200
 AAAAAGTAAAGTGTGACAATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

 a F F I S Q L L F S F I L T I F F D * L E -
 b F S F H S C Y F L L S * Q Y F L I S W K -
 c F H F T A V I F F Y L N N I F * L A G S -

 GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACCTTAGCTTATTCACATTCAT
 1201 -----+-----+-----+-----+-----+ 1260
 CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

 a V K S I K * E K R * T E V T * L I H I H -
 b * K V S N K R S A R L R * L S L F T F I -
 c K K Y Q I R E A L D * G N L A Y S H S * -

 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
 1261 -----+-----+-----+-----+-----+ 1320
 TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTTT

 a R S T F I Y P I R * * G N S S H P F * K -
 b D R P S Y I Q Y D D K E T A V I R F K N -
 c I D L H I S N T M I R K Q Q S S V L K I -

 TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
 1321 -----+-----+-----+-----+-----+ 1380
 ATCAGGATACTCCTGATTTAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

 a * C Y E D * I F R V K K W S R N L N Q K -
 b S A M R T K F L E S R N G A E I L I K K -
 c V L * G L N F * S Q E M E P K S * S K R -

FIG. 35
 (CONTINUED)

1381 GAATTGCGTCGATATTGCAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
 -----+-----+-----+-----+-----+ 1440
 CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGGT
 a E L R R Y C K R I E L * I F R * * V L P -
 b N C V D I A K E S N S K S F V N K Y Y Q -
 c I A S I L Q K N R T L N L S L I S I T N -
 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
 1441 -----+-----+-----+-----+ 1500
 TAGAACTAACTAATTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT
 a I L I D C R D C R G N C T E D H * R N K -
 b S * L I E E I D E A T A Q K I I K E I K -
 c L D * L K R L T R Q L H R R S L K K * S -
 GTAACCTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
 1501 -----+-----+-----+-----+ 1560
 CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT
 a V T F I N * R I N * I T N I E I S D L Q -
 b * L L L I R E * T K L L I * R S A I F N -
 c N F Y * L E N K L N Y * Y R D Q R S S I -
 TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
 1561 -----+-----+-----+-----+ 1620
 AACTGCTTTATTTTCGACTTGATTTCATCTGTTATTTTTTATGTTTGGAACCAAGTTTTA
 a L T K * K L N * S * T I K N T N L G Q N -
 b * R N K S * T K V R Q * K I Q T L V K I -
 c D E I K A E L K L D N K K Y K P W S K Y -
 ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAATAAAATGA
 1621 -----+-----+-----+-----+ 1680
 TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT
 a I E E G K E D Q L A K E K I R Q * I K * -
 b L R K E K K T S * Q K K K * G N K * N E -
 c * G R K R R P V S K R K N K A I N K M S -
 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
 1681 -----+-----+-----+-----+ 1740
 CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAGTTATTAATAACTTTTCTCCCCAA
 a V Q K * R N K R F I F F N N L L K R G V -
 b Y R S E E I K D L F F S I I Y * K E G F -
 c T E V K K * K I Y F F Q * F I E K R G F -
 TTGGGGTTTTGGGGTTTTGGGG
 1741 -----+-----+-----+ 1762
 AACCCCAAAACCCCAAAACCCC
 a L G F W G F G -
 b W G F G V L G -
 c G V L G F W -

FIG. 35
 (CONTINUED)

Figure 36

2 EVDVNDQADNHGHSALKTCEEIKEAKTLYSWIQVIRCRNOSOSHVKDL 51
 19 ELELEMOENQNDIQVRVK...IDDPKQY...LVNVTAACLLQEGSYODK 62
 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF...STGLMIELIDKCLVELL 100
 63 DERAYITKALL...EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF... 107
 101 SSSDVSORQKLOCFCFOLKGNQLAKTHLLTALSTOKQYFFODEWNQVRAM 150
 108 CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144
 151 IGNELEFRHLYTKYLIFORTSEGLVQFCGNNVFDHLKVNDKFDKKOKGGA 200
 145 FDATEFNKLY...LDRILSODIRKELTFRKCLQRCVRSKF 181
 201 ADMNE PRCCSTCKYNVKNEDHFLNNINVPNWNMMKSRTRIFYCTHF 247
 182 SEFNEYOLGKYCTES...QRKKTFRYLSVTNKQKWQOTKKK... 220
 248 NRNNOFFKKHEFVSNKNNISAMDRAOTIFTNIFRFRIRKKLKDVKIEKI 297
 221 RKENLLTKLOAIKESDKSKRETG...DIMNVEDAIKALKPAVMKKI 264
 298 AYMLEKVKDFNFNYLTKSCPLPENWRERKOKIENLINKTREETSKYYEE 347
 265 AKRONAMK...KHKAPKIPNSTLESKYLTFKD 294
 348 LFSYTTDNKCVTOFINEFFYNILPKDFLTGRNRKNFQKKVKYVELNKHE 397
 295 LKFKCHISEP...KERVYKILCKKYPKTEEEYKAAFQDSASAPFN...PE 338
 398 LIHKVLLLEKINTREISWHQVETSAKHFYFDHENIYVLWKLRLRWIFEDL 447
 339 LACKRMKIEISKTWENELSAKNTAEVWDLISSNQLPYMAHLRLNSN... 386
 448 VVSLIACFFVYTEOQKSYSKTYYYRKNIVDMKMSIADLKKETLAEVQE 497
 387 ILKACVSD... 394
 498 KEVEEWKSLGFAPGKLRLIPKKTFRPIMTFNKKIVNSDRKTTKLTNT 547
 395 TTHS 398
 548 KLLNSHLHLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGPKL 597
 399 IVINK...ICEPKAVENSKM 415
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIHTAQILKRKNIVID 647
 416 F PLOFFSAIEAVN.EAVTKGFKAKK...RENNMLKGQIEAVKE...VVE 457
 648 SKNFRKKEMKDYFROKFQKIALEGGQYPTLFSVLENEONDLNAKKT LIVE 697
 458 KTDEEKDM...ELEQTEEGEFVKVNEGIGKQYINSIELAIK 496
 698 AKQRYFKKDNLLQPVINICQYNYINFNGKFKYKQTKGIPQGLCVSSILSS 747
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTSHSGGAKKYGSVRTCLECALVLGL 546
 748 FYYATLEESSLGFLRDESMNPENPNVLLMRLTDDYLLITTOENNAVLFI 797
 547 MVKQCEKSSFYIFSSPSSOCNKCYLEVDL... 576
 798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVVEONIVQDYCD 846
 577 PGDELRPMSHOKLLQEKGLGGG...TDFPYECIDWTKNKTHTVD 617
 847 WIGISIDMKTLALMPNINLRIEGLCTLNLNMOTKKASHMLKKLKSFLM 896
 618 NIVILSDHMAEGYSINVRGSSIVNSI...KKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGKYKMOCAKEYKD.HFKKNLAM 945
 654 PNKIF...AVDLECYG...KCLNLGDEFNENNYIKIFGM 687
 946 SSHIDLEVSKIISVTRAFFKYLVCNIKDTIFGEEHYPDFLSTLKHFI 995
 688 SDOI...LKFIKAKQCGA...NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI...KNFALQKIG 717

Figure 37

132 LSTQKQYFFQDEWNOVRAMIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
 1 MSRRNO...KKPQAPIGNETNLDVFLONLEVYKSQIEHYKTOQQOI 43
 179 GNNVFDHLKVNDKFDKKQKGAADMNEPRCCSTCKYNVKNKEDHFLNNIN 228
 44 KEEDLKLKFKNQDODCGNSGNDODDEE.....NNSNKQOELLRRVN 84
 229 VPNNWNHKSRTIRIFYCTHFNRRNQFFKKHEFVSNNKNNISAMDRAQTIFTN 278
 85QIKQOVOLIKK...VGSKEVDLNLNEDENKKN 114
 279 IFRFNRIKKLKDVKIEKIAYHLEKVKDFNFNYLTCKSCPLPENWRERKO 328
 115 GLSEQOVKEEQRLTITEEQVKYQNLVFNMDYQOLDNESGCHRRHRRRETDY 164
 329 KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFESHQOK.....NYVSIYANQKTSYCWLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHLEIHKVLLLEKINTREISWMOVETSAKHFFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSOTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLRLWI..FEDLVVSLIRCFYVTEQOKSYSKTYYYRKN 475
 243 VNFQNNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKHSIADLKKETLAEVQKEVEEWKKS LGFAPGKRLRIPKKTFRP 525
 291 FAVVFSHR.....HLOGIHLOVPCEAFQYLVNSSSOISVKDSOLO 330
 526 INTFNKKIVNSDRKTTKLTNTNTKLLNSHMLKTLKNRMFKDPFGFAVFN 575
 331 VVSFSTDLKLVQ..TNKVQDYFKFLQEFPRLTHVSQAIPVSATNAVENL 378
 576 ODVMKKYEEFVCKWKVQVQPKLF.....FATMDIEKCYDS..VNREK 615
 379 NVLLKKVKH..ANLNLVSIPTQFNDFYFVNLOHLKLEFGLEPNILTKOK 426
 516 LSTFL.....KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEHK 657
 427 LENLILLSIKOSKXKFLRLNFYTYVAQETSRKQILKQATTIKNLKNKNQ 476
 558 DYFRQKFKIALECCQYPTLFSVLEN..EQNDLNAKKTILIVEAKORNYFK 705
 477 ZETPETKOSTPSESTSCMKFFDHLSELTELEDFSVN...LOATOEIY 520
 706 KDNELQPVNICOYNYINFNGKFKYKOTKGIPOGLCVSSILSSFYATLEE 755
 521 ..OSLHKLIRISTNLKXFKLSYKYEMEKSKHOTFIDLKNI...YETLMN 564
 756 SSLGFLRDESKNPNPNVNLMLRLTDDYLLITTOENNAVLFIKLINVSR 805
 565 ..LKRCSVNISNPHGNISYELTN.....KOSTFYKFKLTLNQE 500
 806 ENGFKFMKKLQTSFPLSPSKFAKYCHDSVEEQNIVQDYCOWIGISIDMK 855
 501 LQHAXYTFK..QNEFOFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ 648
 856 TLALHPNINLRIGILCTLNLMOT..KKASHMLKK..KLKSFLMNNITH 901
 649 NVNI.....IASLLYPNNIQKNPFKNPILLFFKQFEQLKNLENVSINC 691
 902 YFRKTI..TTEDFANKTLNKLFI SCGYKYMOCAYEKDHFKNLAMSSH 948
 692 ILDOHILNSISEFLEKNKKIKAFILKRYYLLOYLYDYTKLFTLOQLPEL 741
 949 IDLEVSKIISVT.....RAFFKYLVCNIKDT..IFGEHY 982
 742 NQVYINQOLEELTVSEVHKQVWENHKOKAFYEPLCEFIKESSTLOLIDF 791
 983 PDFFLS..TLNHFIEIFSTKXY..IFNRVCHILKAKEAKLKSODOCOSLIO 1028
 192 DQNTVSDOSIKKILESISESKYHMYLRLNPSQSSSLIKSENEEIOELLK 840

Figure 38

4 DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK... 47
617 NVKSAKIESSSLESLEDIDSLCKSTASCKNLQNVNIIASLLYPNNIOKNP 666
48 LQKQLEFYFSDANLYNDSFLRKLVLKSGEORVE... IETLLH 86
667 FNKPNLLFFKQFEQLKNLENVSNICILDOHILNSISEFLEKNKKIKAFIL 716

Figure 39

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1 MEHDIDLDDIENL...LPNTFNKYSSSCSDKKGCKTLKSGSKSPS... 42
  | | | | | | | | | | | | | | | | | | | | | | | |
491 [ELAIKIAVNKNLDEIKGHTAIFSDVSGSHSTSHSGGAKKYCSVRTCLEC 540
    | | | | | | | | | | | | | | | | | | | | | | | |
    43 LTIPKLQKO      LEFYFSDANLYNDSFLRKLVLKSGEORVEIETLL 85
    | | | | | | | | | | | | | | | | | | | | | | | |
541 ALVLGLMVKORCEKSSFYIFSSPSSOCNKCYL.EVDLPGDEL RPSHQKLL 589
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Figure 41

telomerase p43	LQKQLEEFYSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La	ICHQUBYYEGDENLPRDKELKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQUBYYEGDENLPRDKELKQOI.LLDDGWVPLETMIK
Drosophila La	ILRQUBYYEGDANLNROKELREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKQUBYYSEFNFPYDRSLRTTAEK.NDGWVPISTIAT

Figure 42

1 aactcatta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaatt itagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagt agggttaaga ttgacgatcc taagcaatat ctggtgaacg tcaatgcagc
 241 atgtttgtg taggaaggtg gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt ctgaggtgg ctgagctga tctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgtgt
 421 ccacaagaat actcaacat tcatcgaaa gtacttcaac aaagcagtac tttgcctaa
 481 tgacttactg gaagtctgt aatttgcata ggttctctat atttttagt caactgaatt
 541 caaaaattg tatctgata ggatacttc ataagatatt cgttaggaac tcactttccg
 601 taagtgtta caaagatgag tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcttaactct accttggaaat caaagtactt
 961 gacctcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatcccttgg aaaaaatacc ctaagaccga agaggaaatc aaagcagcct ttggtgattc
 1081 tgcactgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaatt
 1201 ttaagcaat taactccat atatggccat gttacgtaac ttgtctaaac tcttaaaagc
 1261 cgggttttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
 1321 tgagaactcc aagatgtcc ctcttcaatt cttagtgcc attgaagctg ttaatgaagc
 1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaag gtcaaatcga
 1441 agcagtaaaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
 1501 aaccgaagaa ggagaattg ttaagtcaa cgaagggaatt ggcaagcaat acattaactc
 1561 catgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
 1621 tgaacttctc tctgatgtt ctggttctat gagtacctca atgtcaggtg gagccaagaa
 1681 gtatgttcc gttctactt gtctcgagtg tgcattagtc ctgggttga tggtaaaata
 1741 acgttgigaa aagtcctcat tctacatct cagttcacct agtttcaat gcaataagtg
 1801 ttacttagaa gtgacttcc ctggagacga actccgtcct tctatgtaaa aacttttga
 1861 agagaaagga aaacttggg gtggtactga ttccctctat gagtgcattg atgaatggac
 1921 aaagaataaa actcacgtg acaatatcgt tatttgtct gatatgatga ttgcagaagg
 1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
 2041 tgaagtaaat cctaactta aaactttgc agttgactta gaaggttacg gaaagtgcct
 2101 taatctaggt gatgagtca atgaaaacaa ctacatcaag atattcggtg tgagcgattc
 2161 aatcttaag ttcatctcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
 2221 ctttgcctt caaaaaatag gaaaaaagt agtttctga gattcttcta taacaaaaat
 2281 ctacccccac ttttgttt tatgcatag ccattatgaa atttaataa ttatctattt
 2341 atttaagta ctacatagt ttatgtatc cagtctatta gcctattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

Figure 43

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFGDSASAP
FNPELAGKRMKIEISK TWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNLIKAGV
SDTTHSIVTNKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKKGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIKLA VNKNLDEIKG
HTAJFSDVSGSMSTSMMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVLDLPGDEL RPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKT HVDNIVILSD
MMIAEGYS DINVRGSSIVNSIKKYKDEVNPNIKIFAVDLEGY GKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKIGQK

Figure 44

1 tcaatactat taattaataa ataaaaaaa gcaaaactaca aagaaaatgt caaggcgtaa
 61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaat cttagatttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agtcaaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgaigat gaagaaaaca actcaataaa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagttaaat tgataaaaaa agttgggtct aaggtagaga aagatttgaa
 361 ttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aatagggtta gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtggggccca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggttgaaa tatctcatga ccaaaaaa atgtatcaa ttacgccaa
 601 ctaaaagaca icatattgtt ggtggcttaa agattatttt aataaaaaa attatgatca
 661 tcttaatga agcattaaca gactagaac tgaagccgaa ttctatgcct ttgatgatt
 721 ttcaaaaca atcaaaccta ctaataatc ttactagact gtaacatag acgttaattt
 781 tgataaataa ctctgtatac tgcattgct tagattttta ttactactag aaagattcaa
 841 tattttgaat ataagatctt ctatacaag aaattaatat aattttgaga aaattgggta
 901 gctacttgaa actatcttgc cagttgtctt ttctcatgc cacttacaag gcattcattt
 961 acaagttctt tgcgaagcgt tctaatattt agttaactcc tcatcataaa tttagcgttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
 1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtgcct ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
 1201 caagcatgct aatcttaatt tagtttctat ccttacctaa ttcaattttg atttctactt
 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaa
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaa aatcttaaat tttaagatt
 1381 aaactttac acctacgttg ctaagaacac ctccagaaaa cagatattaa aacaagctac
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
 1501 aactccaagc gaaagcaca gtggtatgaa atttttgat catctttctg aattaaccga
 1561 gcttgaagat ttacgcgtta acttgaagc taccgaagaa atttatgata gcttcacaa
 1621 actttgatt agatcaacaa atttaagaa gttcaaatga agttacaaat atgaaatgga
 1681 aaagagttaa atggatacat tcatagatct taagaatatt tatgaaacct taacaatct
 1741 taaagatgc tctgtaata tatcaaatcc tcatggaaac attcttatg aactgacaaa
 1801 taaagattct acttttata aatttaagct gaccttaac taagaattat aacacgctaa
 1861 gtatatttt aagtagaacg aatttaatt taataacgtt aaaagtgcga aaattgaatc
 1921 ttccctatta gaaagcttag aagatattga tagtcttgc aaactattg ctcttgtaa
 1981 aaattacaa aatgttaata ttatcgccag ttgtctctat cccaacaata tttagaaaaa
 2041 tctttcaat aagcccaatc ttctatttt caagcaatt gaataattga aaaatttgga
 2101 aaatgtatct atcaactgta ttctgatca gcatatactt aattctattt cagaattctt
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta
 2221 tcttgattat actaaattat taaaacact tcaatagtt cctgaattaa attaagttaa
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagtt atcaaagaat catcctaac
 2401 ccttagcta atagatttt accaaaacac tgaagtgtat gactctatta aaaagatttt
 2461 agaattata tctgagtcta agtatatca ttattgaga ttgaacctta gttaatctag
 2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
 2581 aggtgtttta gtaaaagcat actataaatt cctctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcatagatag ggtgattaat taaatattag tttaataaa tattaaatat
 2701 tgaattatc ttgtctatt attgaataa tacatacaat agtcaatttt agtgttttga
 2761 atatatatta gttatttaatt tcatatttt aagtaataa ttattttca atcaattttt
 2821 aaaaaatcg

Figure 45

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIQ
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAE
FYAFDDFSQTIKLTNNSYQTVNIDVNFDDNNLCILALLRFLLSLERFNILNIRSSYTRN
QYNFEKIGELLETFVVFSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF
STDCLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL
VSIPTQFNFDYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFYTY
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLFFKQFEQLK
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPE
LNQVYINQOLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFDQNTVSD
DSIKKJLESISESKYHHYLRLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP
LCLPTGTYYDYNSDRW

Figure 46

MKILFEFIQDKLDIDLQTNSTYKENLKC GFHNG LDEILTT CFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFC HS
ANVNV TLLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK
WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR
EAI FPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLSR
QSPKERV LKFII VILQKLLPQEMFGSKKNKGKIIKNLNL LLSLPLNGYLPFDSLLKKL
RLKDFRWLFISDIWFTKHNFENLNQLAICFISWLF RQLIPKIIQTFFYCTEISSTVTI
VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTL SNFNH SKMRIIPKKS NNEFR
IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE
FKQRLLKKFNNVLP ELYFMKFDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN
TNTGV LKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY
IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV
INIKKLAMGGFQKYNAPANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN
NFHIRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF
KDLSINVTQNMQFHSFLQRH IEMTVSGCPITKCDPLIEYEVRFTILNGFLESLSNTS
KFKDNIILLRKEIQHLQAYIYIYIHVN

Figure 47

Oxytricha
Euploies

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

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Figure 48

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
 GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
 TCTAACTACGTGTTTCGCACTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG
 TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
 ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
 TCTTTTTTGGCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
 GTTCCACAGTTTGGTGGGTACATACGCATTGCTTGATTTATTGATCAATTATACAGTAAT
 TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT
 GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
 ACTTACAGAACCAGTGACAAATAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
 TTTTTTCTTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
 GAGAGAAGCTATTTTTTCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
 TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
 GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTGCGATTTGAGTAGGCA
 ATCACCAAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
 AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTTATCAAGAATCTAAATCTTTTATT
 AAGTTTACCCTTAAATGGCTATTTACCATTGTAGTATTGTTGAAAAAGTTAAGATTTAA
 GGATTTTCGGTGGTTGTTCAATTTCTGATATTTGGTTCAACCAAGCACAAATTTGAAAACCT
 GAATCAATTGGCGATTTGTTTCATTTCTGGCTATTTAGACAATAATTTCCCAAATTTAT
 ACAGACTTTTTTTTACTGCACCGAAATATCTTACAGTGACAATTTGTTTACTTTAGACA
 TGACTACTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
 CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
 AATGAGGATTATACCAAAAAAAGTAATAATGAGTTGAGGATTATTGCCATCCCATGCAG
 AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
 CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
 TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
 TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
 CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
 TTTGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
 TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
 TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAACAGCTTT
 GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
 TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
 CAGTCCTAGCCAGGACACATTAATTTTAAACTGGCTGACGATTTCTTTATAATATCAAC
 AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
 TGCGAAAGCCAATAGAGACAAAATTTAGCCGTAAGCTCCAATCAGATGATGATACGGT
 TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
 CACAATGAATAATTTCCATATCCGTTGAAATCTAGTAAAGGATATTTGGAAGTTTAAAT
 AGCGCTGTTTAACTAGAAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
 CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTGGAATGTTATAAATCTGC
 TTTTAAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTATTGTTCTTACAACG
 CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
 TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAGCCTATCTTCAAACACATCAA
 ATTTAAAGATAATATCATTCTTTTGAAGAAAGGAAATTCAACACTTGCAAGC

Figure 49

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHQREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

Figure 50

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAGAAGACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAA
GAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGA
AGCCAGGCCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACG
GGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCG
CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTTCAGC
GTGCTCAACTACGAGCGGGCGCG

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

Figure 52

ggtaaccgattacmccmctcataagctaattgcttccctgaacgctcctaaatctctggaatatmttacaagaactcaataacaataccaagtcaaattccaatatgaagg
tgnattagtgatcgataatattctattttatcggtcggtaccaagtataaggacaaaaagaacaactccttccccctaaagacmttactmttaatttactmccaatatattcg
gggtcggtactmttaacgtgggtactgtggtacttctgacccaaccggtgtttctaccccgicattggatagctcttggagtagctcacagaaatccttacaaatctt
ctgatgagactatattagattcattacagtcggtgcataattcttaacatggagccttacacttttagatgagtcacgtcgcatgattggagatttggatcatccaacgtrtgcctg
aaaagggtgataattatmgcaaaatcagtcccttagtgggtgaaatccgcgaaagtttttgatgcttgcacacgcttagcatgattgagatattcaaaaatttctatccactacaa
ctcctttaacgcgggtttattttctattmctatttctcatgttgttccaaatatgtatcatctcgtattaggcgtttttccgttttactcctggaaatgtaacatttattagctatcattatataaaa
aataatctaattagttcgcttaattgatagtagtagaagattgggtgattctactcgtgaattgttattagtttaagatactttgcaaaacatttattagctatcattatataaaa
aaaatcctataattataaataattaatatttgcgggtcactatttttaaaacggtatgatcagtaggacactttgcatatataatgattgcttaattgggtactgttaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAAATCAATATGTATACCTATGTA
CCTTAAATGATTATGTACAACCTTGTGTTTGAAGGGTGCCTCGGCAAGCTCGTATAGCAATATATGCGAA
CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTCTTCATTGACTGTAGTCGGCTTCGACAGT
AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatatatmttggtttggatttttctattcg
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ATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGCTCTGCAGAAGTCAA

[illegible]

Figure 53

EST2 pep	FFYCTEISST	VTIVYFRHDT	WN----	KLIT	P-----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQQKS	YSKTYYYRKN	IWDVI-MKMS	IAD----	LKK	ETLA--EVQE		43
Trans of tetrahymen	-----KHKE	GSQIFYRKP	IWKLVSKLTI	VKVRIQFSEK	NKQMTQNFYQ			44
Consensus	FFY.TE..K.	.S..YYRK.	IW...-KL..F..KV..			50
EST2 pep	NVCRNHNSY-	-----	TLSNFNHNSKM	RIIPKKSNN	FRITAI	PCRG		79
Euplotes pep	KEVEEWKSL	-----	---GFAPCKL	RIIPKKT--	FRHIMTFNKK			78
Trans of tetrahymen	KIQLEEENLE	KVEEKLIPE	SFOKYPOCKL	RIIPKKS--	FRHIMTFLRK			92
Consensus	K...E.....	-----F..GAL	RIIPKKS--	FRHIMTF.RK			100
EST2 pep	ADEESFTIYK	ENHQNAIQPT	QKILEYLRNK	RPTSFTKIYS	PTQIADRIKE			129
Euplotes pep	IVNSDRKTTK	LTTNTALLNS	HLMLKTLRN-	-----RMFK	-D2FGFAVEN			120
Trans of tetrahymen	DKQKNIK---	LNLNQILMDS	QLVFRNKD-	-----ML-G	-QXIGYSVFD			130
ConsensusK..K	LN.N..L..S	QL.L.L..LRN-	-----	...IG..VF.			150
EST2 pep	FKORLLKGEN	NVL-----	FEILFMKFD	VKSCYD				157
Euplotes pep	YD-DVMKQVE	EFVCKWKQVG	QKLEFFATMD	TEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWQKNG	RECELYVTL-	-----				158
Consensus	.K-...KLF.	.F..KWK..G	ELKLF.T.D	...CYD				186

Figure 54

S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q .
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

Figure 55

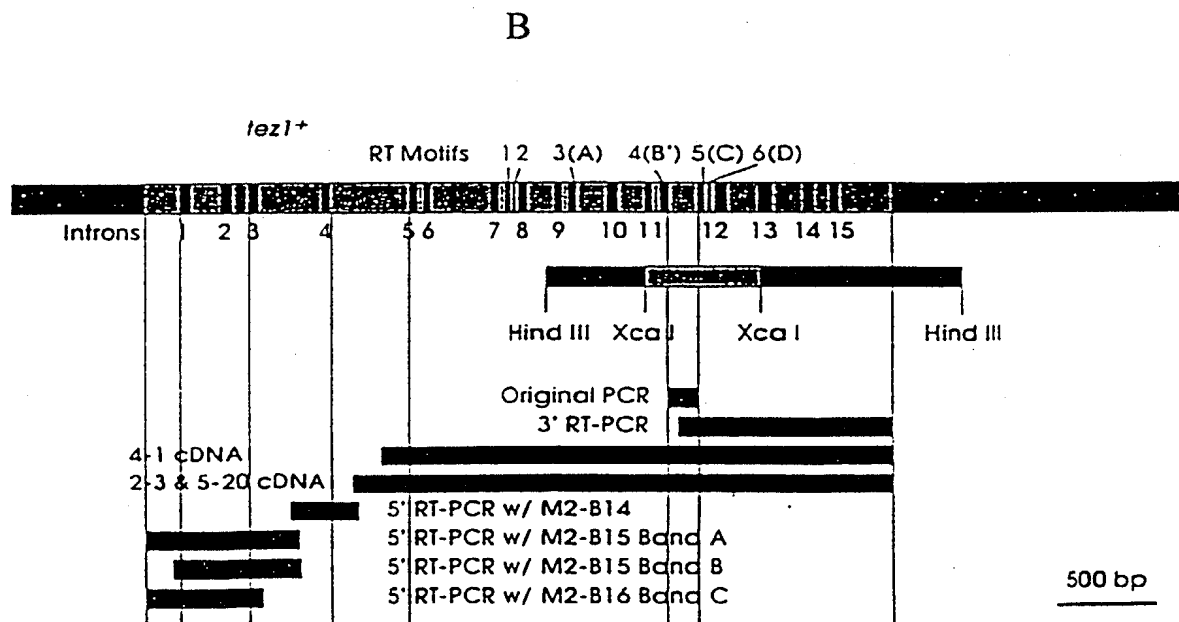
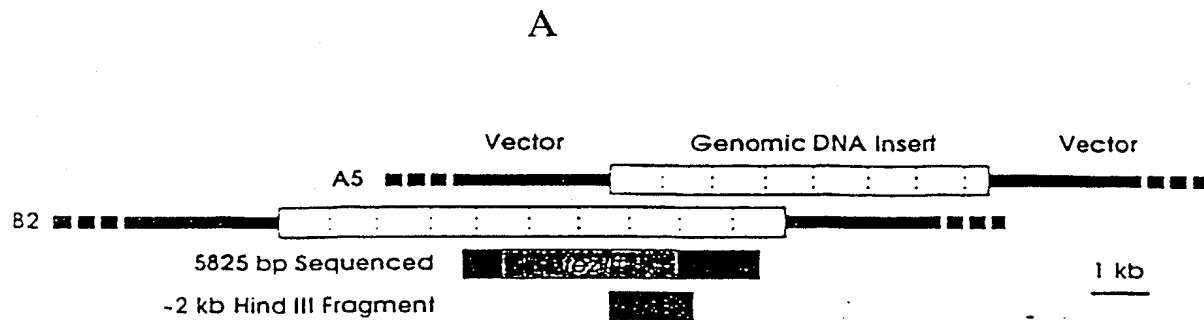


Figure 56

Poly 4

			t		t		c		
	t	a	a	g	c	c	t	c	g
5'-	cag	acc	aaa	gga	att	cca	taa	gg	-3'
	Q	T	K	G	I	P	Q	G	

4 (B')

5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	
			t	t	t	t	t	
					c	c		

Poly 1

Figure 57

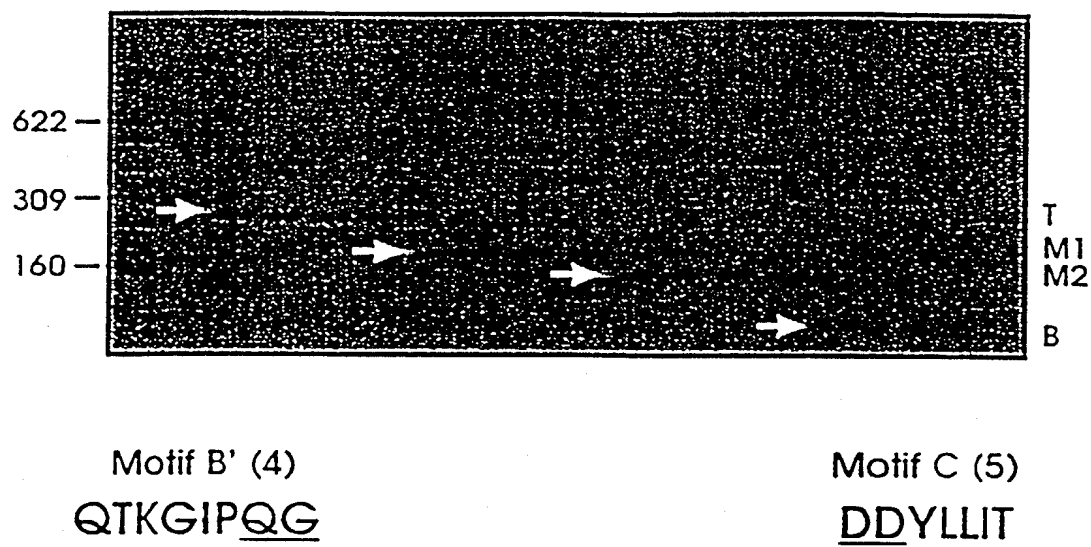


Figure 58

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

```

Ot          LCVSYILSSFYYANLEENALQFLRKESMDPEKPEKNLLMRLT
Ea_p123     KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2       SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103     DGLFQGSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS
            . * . * . * . . . . .

```

```

Q K V G I P Q G
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

```

Poly 4

```

      t      t      c
c a a g c c t c g
cag acc aaa gga att cca taa gg ---->
cag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
cc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

      K G : P S G S I L S S F L C H F Y M

```

```

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

```

```

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

```

```

V V D D Y L L I T

```

```

<--- ctg ctg atg gag gag tag tgg
      a a a a a a a a
          t t t t
              c c

```

Poly 1

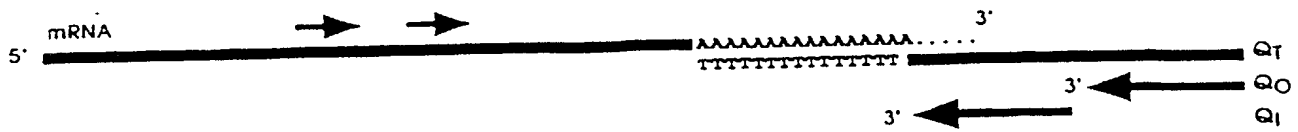
```

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.
D D F L F I T

```

Figure 59

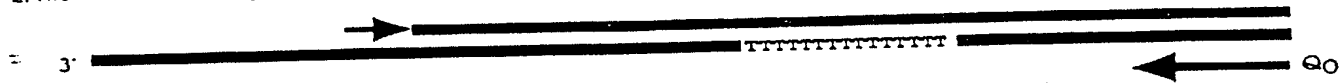
3' RT PCR Strategy



1. Synthesis of cDNA with Q_T Primer.



2. First Round PCR Using Outside Primer and Q_O Primer.



3. Second Round PCR Using Inside Primer and Q_I Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.

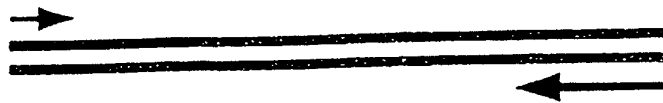


Figure 60

A

-Size Selected Libraries from P. Nurese

- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

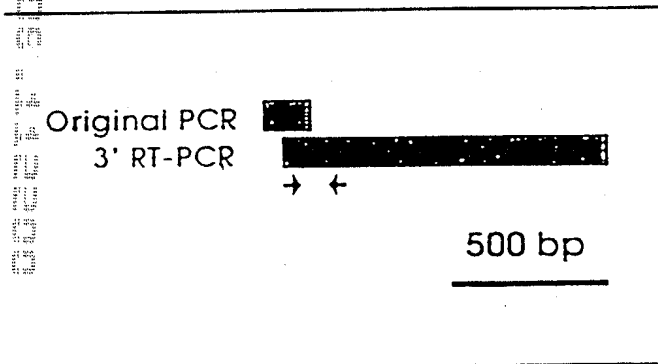
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

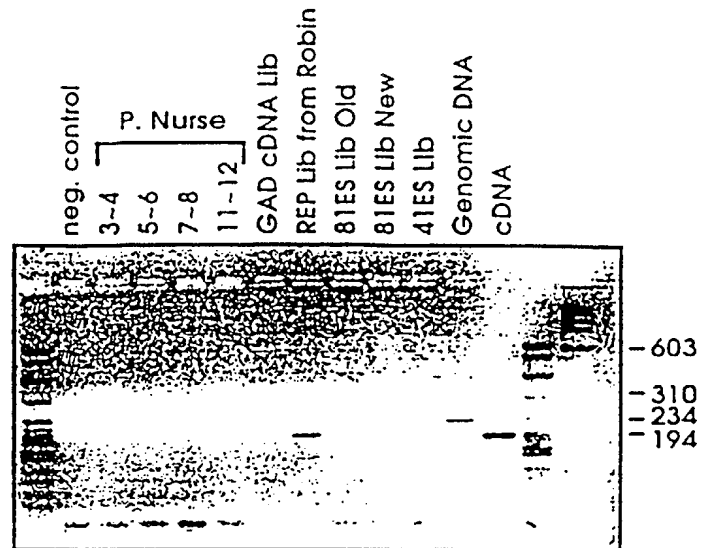
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B



C



D

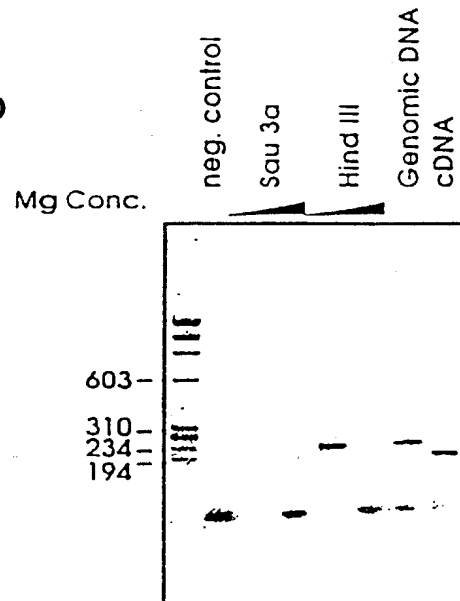
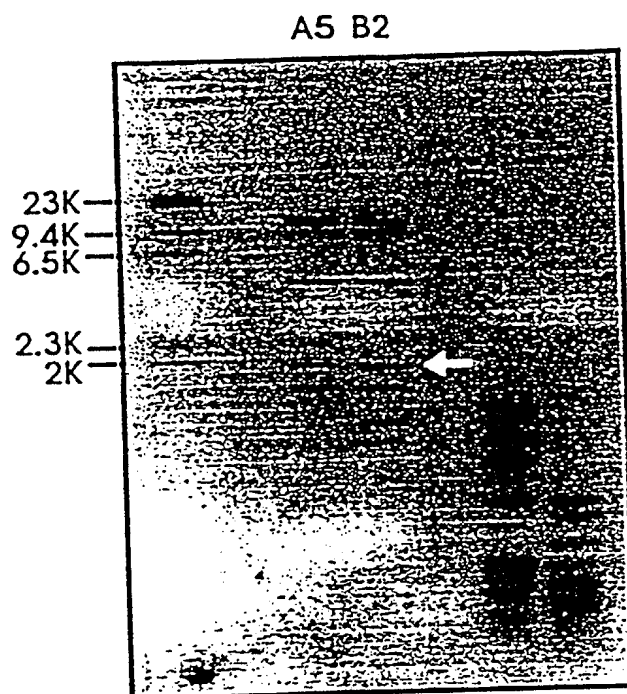
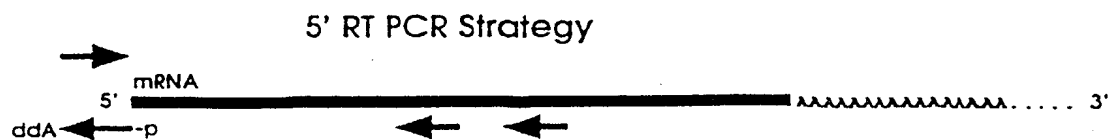


Figure 61



Hind III Digested Positive Genomic Clones

Figure 62



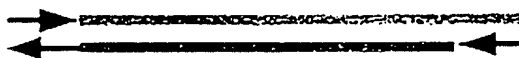
1. Synthesis of cDNA with Specific Downstream Primer.



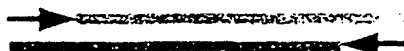
2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

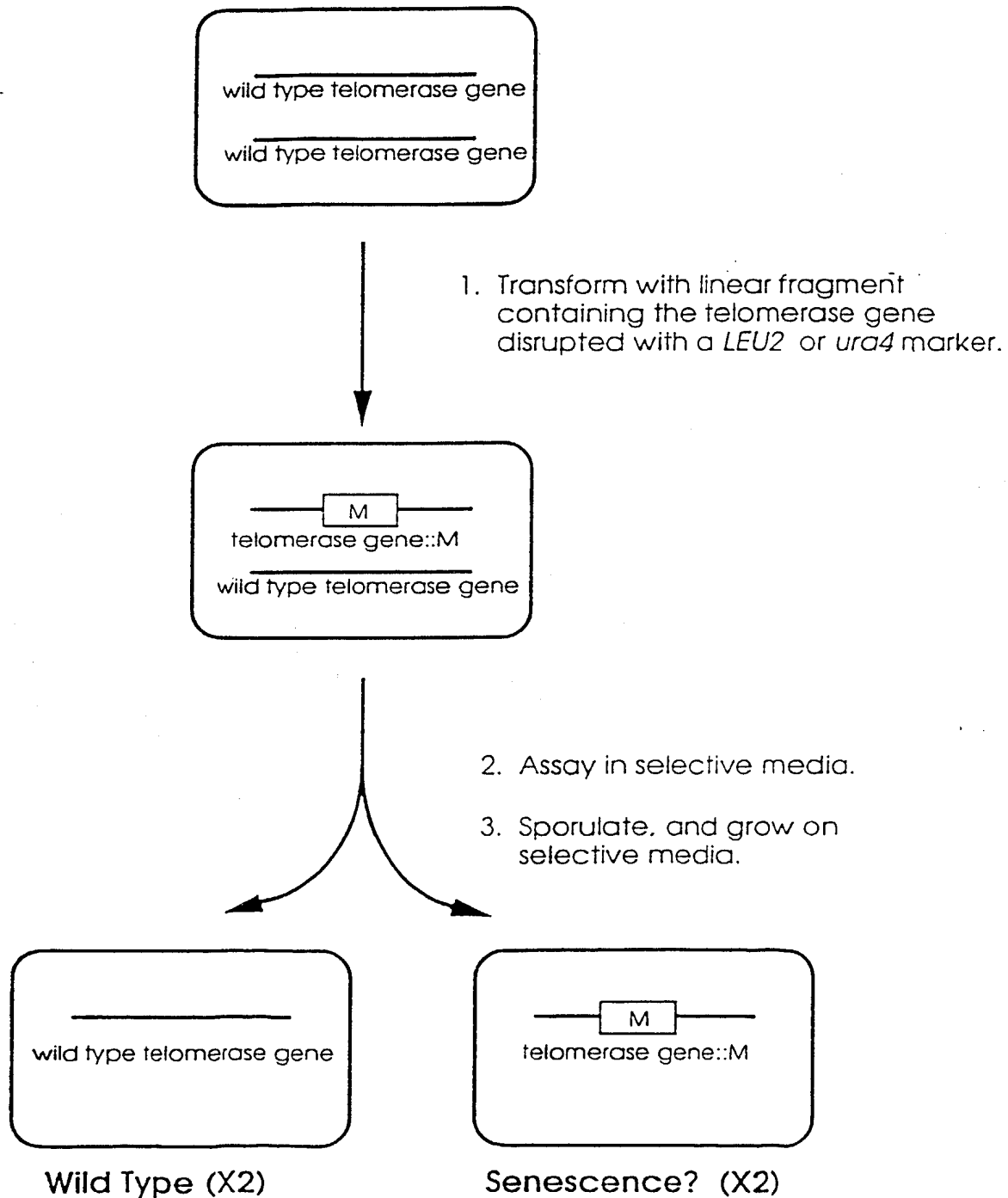


B

Seq_Tuple 1MTENHTPKSRILAFLENOVYVLCST 1
Seq_Contig 1MKELFEPF 1
Ca_p123 1 MEVDYVQGAADMGHNSALETKIEAKLYTSW 1
Seq_Tuple 2 M.....LVQVLYLVLRGSPAL.....SNICERLAEEDVOTSF 2
Seq_Contig 2 1 FODKLDLIDGL.....NLKCEGHNFHOLD 2
Ca_p123 2 LQKYLIRKGRQSD.....OLEDTFFAOTW 2
Seq_Tuple 3 1 FLKSTVYVQFOSKPDQGVQVFSPPKCSQSESL 3
Seq_Contig 3 1NLTCEHLEKHLK 3
Ca_p123 3 VVATPRTVHESEQFVIAKVEVFTSLGMIFL 3
Seq_Tuple 4 1 VYKQMFQCEVFERR.....NLMK.....PSMNHQOFKRAMN 4
Seq_Contig 4 1NLTCEHLEKHLK 4
Ca_p123 4 CLVELLSDDSDVSDOROKLOCF.....FOLKGN 4
Seq_Tuple 5 1 VYQVHOLVETFRPHVLSILEKSLGOLLLEIF 5
Seq_Contig 5 1VYQVHOLVETFRPHVLSILEKSLGOLLLEIF 5
Ca_p123 5LAKTLMTALSTOKQVFFOODSNOVRAM 5
Seq_Tuple 6 1 SDAMNYLKGKSIFEALPHQWYLSIFLFLFK 6
Seq_Contig 6 1 VYAFV.....HYHTYVQF.....GOFFTV 6
Ca_p123 6 NELFRN.....YTKYLIFQWTSQGLV.....NHNVFVD 6
Seq_Tuple 7 1 VYFETVYKCKRKATITSTYON.....KSARKK 7
Seq_Contig 7 1VYFETVYKCKRKATITSTYON.....KSARKK 7
Ca_p123 7 LKYNDFVK.....RSGSSATAAQT.....KOLTEP 7
Seq_Tuple 8 1 WMSISIRSFIFVRSBYKFKOOLVFNHLSIC 8
Seq_Contig 8 1WMSISIRSFIFVRSBYKFKOOLVFNHLSIC 8
Ca_p123 8 NEK.....DHFLLNNHVFPMWMMESRTIFCYCTHN 8
Seq_Tuple 9 1 ANTYHMLWNIWFPFOLINAFQVKNLKEVPL 9
Seq_Contig 9 1NTYHMLWNIWFPFOLINAFQVKNLKEVPL 9
Ca_p123 9NHQFFKEHEFVNKNHNISAMORAOT 9
Seq_Tuple 10 1 VS.....OSTVYPRKLLVYVPLIEQTAKLHRI 10
Seq_Contig 10 1 IN.....LVYPRKLVRIMLLOKLKMERKL 10
Ca_p123 10 STNIFRPHIRKLEKQVIEKIAMYLEVYKQFM 10
Seq_Tuple 11 1 LSKYNNHT.....VID.....HODEKILSYELEKPH 11
Seq_Contig 11 1 VYSLTSL.....PLEGTVDLHSLNOSPKE 11
Ca_p123 11 ANYTLTSL.....LPHEWRERKSLNHLNKTREEK 11
Seq_Tuple 12 1LAKLRSILVYVLEIF 12
Seq_Contig 12 1 SKYVEELSYVYTON.....LFL.....VILVOKLLDEM 12
Ca_p123 12 SKYVEELSYVYTON.....LFL.....VILVOKLLDEM 12
Seq_Tuple 13 1 WGNORIFEIIL.....DLETKL.....RYEVSFLNY 13
Seq_Contig 13 1 FTGKRNKQKIL.....MLNLLSL.....PLNGTLPFOSL 13
Ca_p123 13 LQK.....RNRKQF.....VKKVYV.....NEMELHNLRL 13
Seq_Tuple 14 1 NIKISEIETLVQGRNKNKCLDSQKQKQIFA 14
Seq_Contig 14 1 KRLKQF.....LVLS.....OIVYKHNPLNHLOLA 14
Ca_p123 14 KINTREISLNOVETS.....AKHFVYFON.....LYVLW 14
Seq_Tuple 15 1 ERYVLYTNFSILPILOS.....SSDLNRYTV 15
Seq_Contig 15 1 CFISLFLFROLPIKQIOT.....CISLSTYV 15
Ca_p123 15 ELRLIFEDLYVSLIKR.....VLOKSTSYKTE 15
Seq_Tuple 16 1 FKDIKLLCRPPFYSMEKEAFKIEHNHYND 16
Seq_Contig 16 1 FKHOTNKLITPPVEYKPTLVYHNHNHNS 16
Ca_p123 16 YKHIDYVFMKMSADLKEKTLAEQVEYEW 16
Seq_Tuple 17 1 FOETLTPPAVILL.....MTLTLRLKRL 17
Seq_Contig 17 1 TFLTHFNKSKL.....SMKEKLAIFIRGAD 17
Ca_p123 17 EKSLQFAQKLL.....ITTT.....NHNKIL 17
Seq_Tuple 18 1 IKMOENKMLVSYTNOFLTPVARSILKHE..... 18
Seq_Contig 18 1 EER.....VYFQFQKQIFQFQKQIFQFQKQIF 18
Ca_p123 18 HSD.....RKTKETLTKLLHNSLLEKTR 18
Seq_Tuple 19 1 ESSDIPFNLEVYMKLLTFKCOLLHNMFQNK 19
Seq_Contig 19 1ESSDIPFNLEVYMKLLTFKCOLLHNMFQNK 19
Ca_p123 19 KQPPQFAVFNHYDQVMEKEEYFVCKVQVQPL 19
Seq_Tuple 20 1 VYVRIK.....RIKQOLNPIV.....KLEKQPE 20
Seq_Contig 20 1VYVRIK.....RIKQOLNPIV.....KLEKQPE 20
Ca_p123 20 FATH.....VKNREKSTFLTKKLSO 20
Seq_Tuple 21 1 VIKYATINATSDRAK..... 21
Seq_Contig 21 1 FVNSQFFQK..... 21
Ca_p123 21 WIMTAQILKRNKNIYOSKFRKEMEDFYQK 21
Seq_Tuple 22 1 FYSEAFSEYFQWVPPFVQLLS.....KETSDF 22
Seq_Contig 22 1FYSEAFSEYFQWVPPFVQLLS.....KETSDF 22
Ca_p123 22 FQKIALGEOQVPTFL.....LENEOHLNKEKIV 22
Seq_Tuple 23 1 OFVDVYWKSSSEIFKNLKEHLSOHVKEIGNSO 23
Seq_Contig 23 1 ONRVTYHLSHODVYVNVMEIKTALVYEOCK 23
Ca_p123 23 EAKQRNVTFKQDHLQPLVIFICQYTHIFNQK 23
Seq_Tuple 24 1 LQKYVIFLCLVIFLFLCHYFMEIDETLSYTK 24
Seq_Contig 24 1 IREDLFLFCLVAPVIVOLYVQLEFYSEKAL 24
Ca_p123 24 KOTEKIFLCLVLSISLFFVATTEESLSALR 24
Seq_Tuple 25 1 KEG.....SVLLRV.....TVUEKEDIN 25
Seq_Contig 25 1 SPQOO.....TLIKLAL.....STOQOOYK 25
Ca_p123 25 DCSMHPNPNHVLNHLVLT.....TTOGHNVL 25
Seq_Tuple 26 1 FLNLQYKQFKNHASTSLTVINFERNG..... 26
Seq_Contig 26 1 IKELANGQYQKYNKANOILATYSSD..... 26
Ca_p123 26 FIEKLINVSRENGYFQFNNLLOSTFPLPSKFA 26
Seq_Tuple 27 1LIMHTFSEKRRMPPQFVNMHSLDILL 27
Seq_Contig 27 1ODTVIOFCA.....MHVPEKLEWMSSTIM 27
Ca_p123 27 KYQMSVEEQNIYQDVQDWIGISIDMKETLAP 27
Seq_Tuple 28 1 AKCIDAEALFVSVELTNHMGGSFFVILRSS 28
Seq_Contig 28 1 HNFHISSESSKGIIFSLIALFRIESTIDIT 28
Ca_p123 28 NMLRIEIGLICLNLNMWFKCASMMLKELSF 28
Seq_Tuple 29 1 ASAFQVFIIDTHNSESCKRIYLGYSNCHM 29
Seq_Contig 29 1 NRSNTVYLMQIDHNVKNISCK 29
Ca_p123 29 MNNHITHYRKTITTEOFANALNKLFSQGT 29
Seq_Tuple 30 1 AQATLKR.....LIPFORMITOLLNVIOKREK 30
Seq_Contig 30 1YKRAF.....LSPIN.....VIONMHQNSFLQ 30
Ca_p123 30 FMQCAKE.....NPKHMLAMSIOLEVS.....YV 30
Seq_Tuple 31 1 LAELIOTYSRPLSAEYVFWFLCLOMNGKPS 31
Seq_Contig 31 1 FVSDGPIKQKLFIEVFNATLHNPDCLESM 31
Ca_p123 31 TRAFFYFLVCHIKOTIFGEHNFQPLST 31
Seq_Tuple 32 1 FYHPCFEOLIV.....OLSTOLFLPLRN.....QVLY 32
Seq_Contig 32 1 FS.....KADNVHLLAKEKAKAKSOOC 32
Ca_p123 32 ICFSS.....TCKVILKNVCHILKA 32
Seq_Tuple 33 1 LNRRIAD 33
Seq_Contig 33 1OYDA 33
Ca_p123 33OYDA 33

Figure 65

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

Figure 66

An Example of Confirmation of *tez1* disruption By PCR

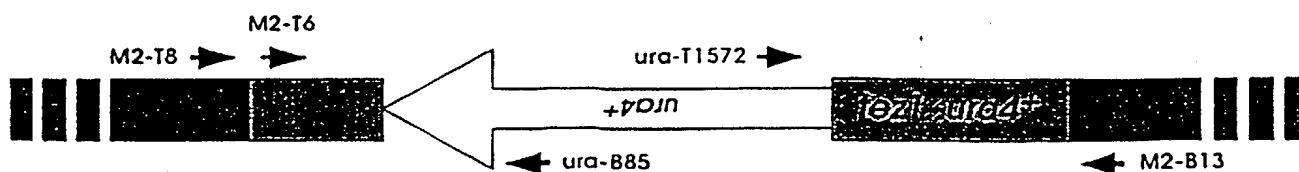
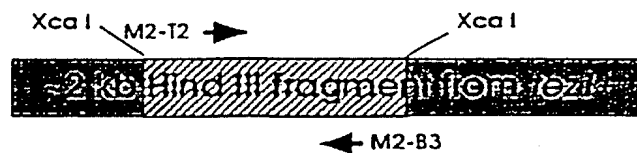
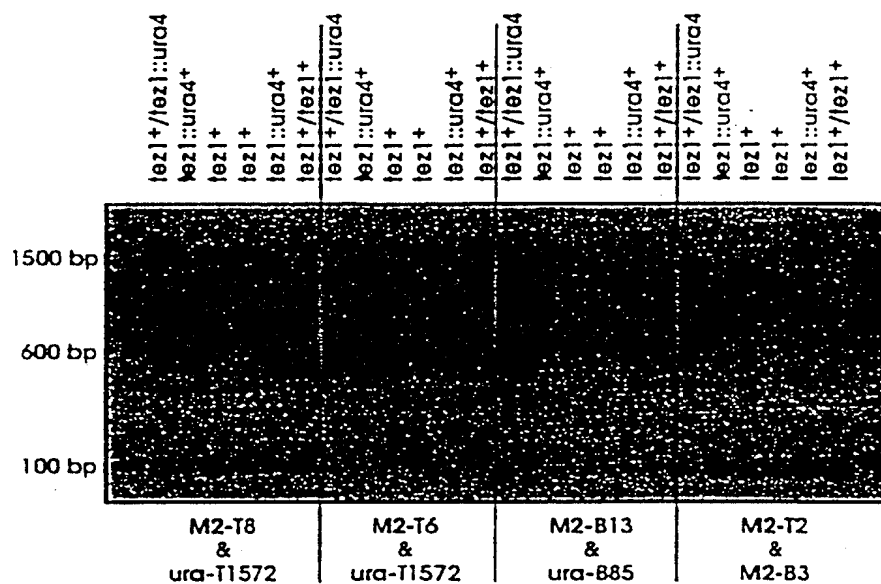
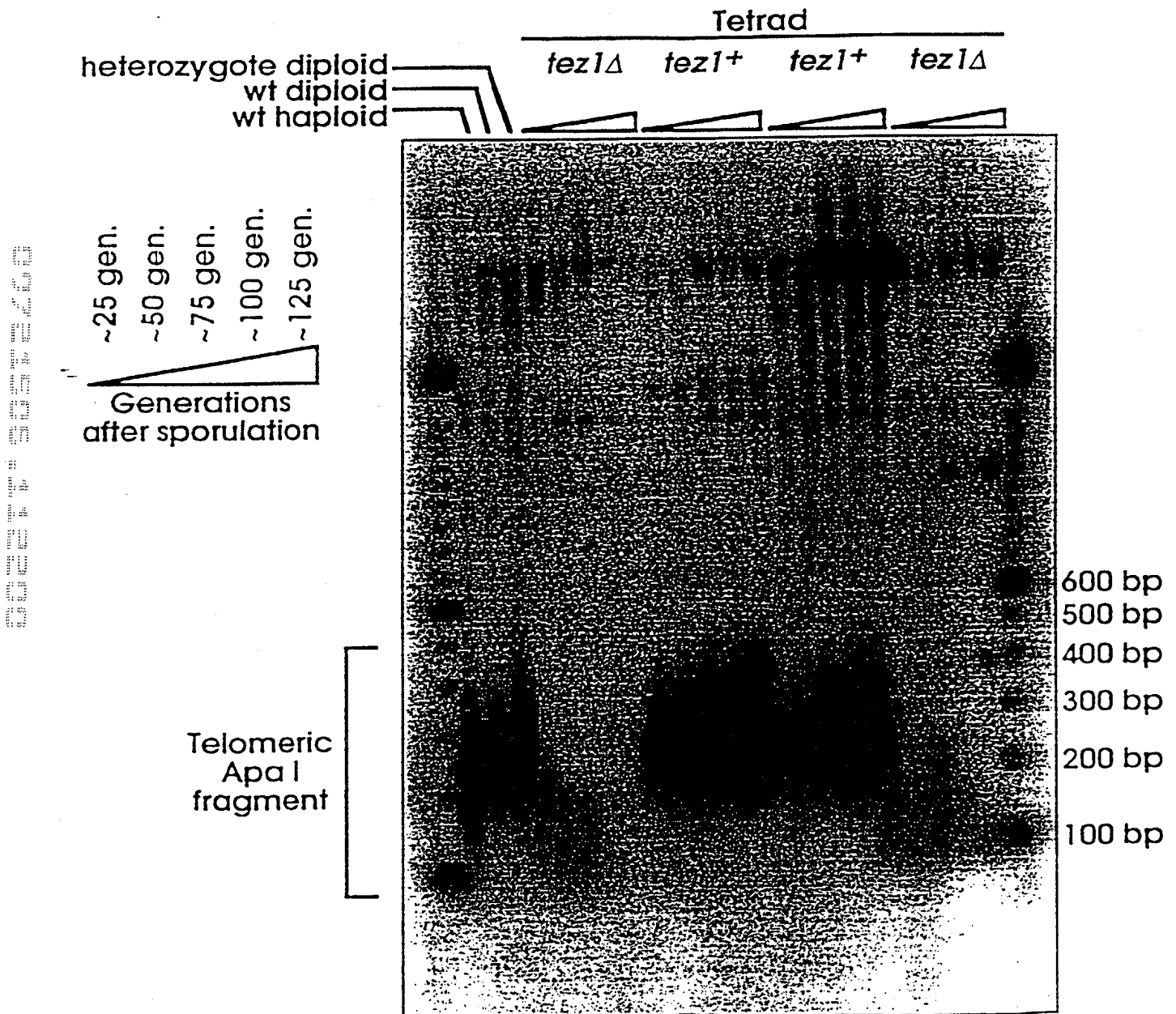


Figure 67

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*





						1	met	ser	val	tyr	val	val	glu	leu	leu
GCCAAGTTCCTGCACTGGCTG						ATG	AGT	GTG	TAC	GTC	GTC	GAG	CTG	CTC	
10											20				
arg	ser	phe	phe	tyr	val	thr	glu	thr	thr	phe	gln	lys	asn	arg	
AGG	TCT	TTC	TTT	TAT	GTC	ACG	GAG	ACC	ACG	TTT	CAA	AAG	AAC	AGG	
30															
leu	phe	phe	tyr	arg	lys	ser	val	trp	ser	lys	leu	gln	ser	ile	
CTC	TTT	TTC	TAC	CGG	AAG	AGT	GTC	TGG	AGC	AAG	TTG	CAA	AGC	ATT	
40											50				
gly	ile	arg	gln	his	leu	lys	arg	val	gln	leu	arg	glu	leu	ser	
GGA	ATC	AGA	CAG	CAC	TTG	AAG	AGG	GTG	CAG	CTG	CGG	GAG	CTG	TCG	
60															
glu	ala	glu	val	arg	gln	his	arg	glu	ala	arg	pro	ala	leu	leu	
GAA	GCA	GAG	GTC	AGG	CAG	CAT	CGG	GAA	GCC	AGG	CCC	GCC	CTG	CTG	
70											80				
thr	ser	arg	leu	arg	phe	ile	pro	lys	pro	asp	gly	leu	arg	pro	
ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	AAG	CCT	GAC	GGG	CTG	CGG	CCG	
90															
ile	val	asn	met	asp	tyr	val	val	gly	ala	arg	thr	phe	arg	arg	
ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	GCC	AGA	ACG	TTC	CGC	AGA	
100											110				
glu	lys		ala	glu	arg	leu	thr	ser	arg	val	lys	ala	leu	phe	
GAA	AAG	ARG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	GTG	AAG	GCA	CTG	TTC	
120															
ser	val	leu	asn	tyr	glu	arg	ala	arg	arg	pro	gly	leu	leu	gly	
AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	GGC	CTC	CTG	GGC	
130											140				
ala	ser	val	leu	gly	leu	asp	asp	ile	his	arg	ala	trp	arg	thr	
GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	TGG	CGC	ACC	
150															
phe	val	leu	arg	val	arg	ala	gln	asp	pro	pro	pro	glu	leu	tyr	
TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	CTG	TAC	
160											170				
phe	val	lys	val	asp	val	thr	gly	ala	tyr	asp	thr	ile	pro	gln	
TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC	CAG	
180															
asp	arg	leu	thr	glu	val	ile	ala	ser	ile	ile	lys	pro	gln	asn	
GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG	AAC	

Figure 68 (cont.)

190	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	200	gln	lys	ala	ala	met
	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC		CAG	AAG	GCC	GCC	ATG
	gly	thr	ser	ala	arg	pro	ser	arg	ala	thr	210	ser	tyr	val	gln	cys
	GGC	ACG	TCC	GCA	AGG	CCT	TCA	AGA	GCC	ACG		TCC	TAC	GTC	CAG	TGC
220	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	230	thr	leu	leu	cys	ser
	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC		ACG	CTG	CTC	TGC	AGC
	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	240	phe	ala	gly	ile	arg
	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG		TTT	GCG	GGG	ATT	CGG
250	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	260	asp	phe	leu	leu	val
	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT		GAT	TTC	TTG	TTG	GTG
	thr	pro	his	leu	thr	his	ala	lys	thr	phe	270	leu	arg	thr	leu	val
	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC		CTC	AGG	ACC	CTG	GTC
280	arg	gly	val	pro	glu	tyr	gly	cys	val	val	290	asn	leu	arg	lys	thr
	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG		AAC	TTG	CGG	AAG	ACA
	val	val	asn	phe	pro	val	glu	asp	glu	ala	300	leu	gly	gly	thr	ala
	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC		CTG	GGT	GGC	ACG	GCT
310	phe	val	gln	met	pro	ala	his	gly	leu	phe	320	pro	trp	cys	gly	leu
	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC		CCC	TGG	TGC	GGC	CTG
	leu	leu	asp	thr	arg	thr	leu	glu	val	gln	330	ser	asp	tyr	ser	ser
	CTG	CTG	GAT	ACC	CGG	ACC	CTG	GAG	GTG	CAG		AGC	GAC	TAC	TCC	AGC
340	tyr	ala	arg	thr	ser	ile	arg	ala	ser	leu	350	thr	phe	asn	arg	gly
	TAT	GCC	CGG	ACC	TCC	ATC	AGA	GCC	AGT	CTC		ACC	TTC	AAC	CGC	GGC
	phe	lys	ala	gly	arg	asn	met	arg	arg	lys	360	leu	phe	gly	val	leu
	TTC	AAG	GCT	GGG	AGG	AAC	ATG	CGT	CGC	AAA		CTC	TTT	GGG	GTC	TTG
370	arg	leu	lys	cys	his	ser	leu	phe	leu	asp	380	leu	gln	val	asn	ser
	CGG	CTG	AAG	TGT	CAC	AGC	CTG	TTT	CTG	GAT		TTG	CAG	GTG	AAC	AGC

Figure 68 (cont.)

390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGT TTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

Figure 68 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTACCCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTACAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 69

Motif -1
 Ep p123 ...LVVSLIRCFFYVTEQQKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESSDLRNRT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRRLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPAPAVIRLLPKKN--TFRLITNLRKRFL...
 Sc Est2 ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
 consensus R PK R I

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFVDVKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFEEKHNFST...
 Sc Est2 ...KKLAMGGFQKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

Figure 70

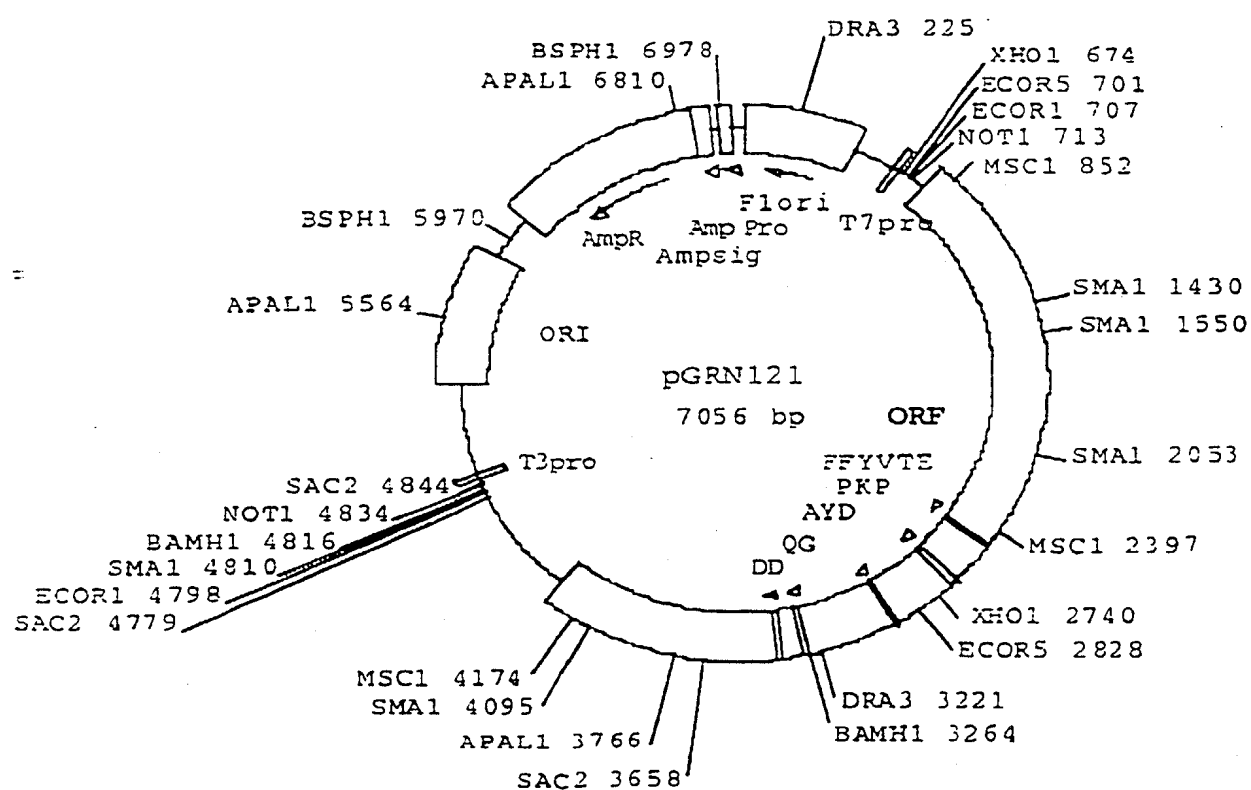


Figure 71

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCC CGAGGCCTTC
 401 ACCACCAGCG TGC GCAGCTA CCTGCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGGC GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGC GCGNTNT TTGTGCTGGT GGNTCCCAGC
 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCCG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCTT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTCCCCAAG AGGCCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCTTGG GCCACCCGG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCCTCTAC
 1051 TCCTCAGGCG ACAAGNACAC TGC GNCCTC CTTCCTACTC AATATATCTG
 1101 AGGCCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCGC AGGTTGCCCC GCCTGCCCCA
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAAACCAG
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCCGAGGAGG AGGAACACAG ACCCCCGTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TCGGGGACTG
 1601 CGCTTGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTC TGGAGCAAGT
 1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTCCGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCCGCAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

Figure 71 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TCGGTTTGGT
2651 GGATGATTTT TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
2801 GGCTTTTGTG CAGATGCCGG CCCACGGCCT ATTCCCCTGG TGCGGCCTGC
2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
2901 CGGACCTCCA TCAGAGCCAG TCTCACCTT AACC GCGGCT TCAAGGCTGG
2951 GAGGAACATG CGTCGAAAC TCTTTGGGGT CTTGCGGCTG AAGTGTCA
3001 GCCTGTTTCT GGATTGTCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
3101 GCAGCTCCA TTTTCATCAGC AAGTTTGGA GAACCCCA TTTTCCTGC
3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCACTCAG GACAGCCCAG
3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
3601 CCGGCTGAAG GCTGAGTGTC CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCCA CAGGCTGGCG
3701 CTCGGCTCCA CCCCAGGGCC AGCTTTTCCT CACCAGGAGC CCGGCTTCCA
3751 CTCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
3901 TACACAGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
3951 GGGGGGAGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT
4001 TTGAAAAAA AAAAAAAAAA AAAAAAAAAA

GCAGGGCTGGCTCCTGCTGGCGCAGGTGGGAAGTCCCTGGTCCCGGCCACCCCTGGGATGCC

[illegible]

Figure 72 (cont.)

TGGATCGAGTGAACCTGGTTTCTGTGTGTGTACCTCCGACAGCCCTCCCAAGAAAGCCAC
 841 ----- 900
 ACCTGAGCTCACTGGACCAAGACACACACAGTGGAGGGTCTGGGCGGCTTCTTCCCTG
 A
 W T E * P W F L C G V T C Q T R R R S H -
 b
 G P S D R G F C V V S P A R P A E E A T
 c
 D R V T V V S V W C H L P D P F K K P F -
 CTCTTTGGAGGGTGGGCTCTGTGGCAGCGGCACTCCACCCATCGGTGGGCGGCGAGCA
 901 ----- 960
 CAGAAAGCTCCACCGGAGAGACCGTGGCGGTGAGGGTGGGTAGGCACCCGCGGCTCCT
 A
 L F G G C A L W H A F L F P I R G F F A
 b
 S L E G A L S G T K H S H P S V G R Q H -
 c
 L W R V R S L A R A T P T H P W A A S T -
 CCAGCGGCGGCGGCTTCCACATCGGCGGCGGCGGCTTGGGACACGCTTGGTCCGCTG
 961 ----- 1020
 GGTGGCGGCTGGGCGGCTAGGCTGTAGCGCGGCTGGTGGCAGGAAGCTGTGGCGGACAGGCGG
 A
 P R G P P I H I A A T T S W D T F C P P
 b
 H A G P P S T S R P P R P G T R L V P E
 c
 T R A F H P H R G H H V L G H A L S P G -
 GTGTAGCGGAGACCAAGCACTTCTCTACTCCTCAGGCGGACAAGNACACTGGGCGGCTT
 1021 ----- 1080
 CACATGGGCTGTGTGTGTGTGTAGGAGATGAGGAGTCCGCTGTTCNTGTGAAGGCGGAG
 A
 V Y A E T K H F L Y S S C D K ? T A ? L -
 b
 C T P R P S T S S T P Q A T ? T L R P S -
 c
 V R R D Q A L P L L L R R Q ? H C ? P P -
 CTCTACTCTCAATATATCTGAGGCGGCGGCTGACTGGCGGTTGGGAGGTTTGTGGAGACA
 1081 ----- 1140
 GAAGATGAGTTTATAGACTTGGGCTTGGGAGTACCGCAAGGCTTCAAGGCACTTCTCT
 A
 L P T Q Y I * G P A * L A F G R F V E T
 b
 F L L N I S E A O P D W R S G G S W R Y -
 c
 S Y S I Y L R P S L T G V R E V R G D ? -
 NTCTTCTGTGTTCAGGCGCTTGGATGCGAGGATTCGCGGAGGTTGGCGGCGCTGCGGCA
 1141 ----- 1200
 NAGAAAGAGCAAGGTTTGGCAACTTACGCTTCTAAGGCGGCTTCAAGCGGCGGAGCGGCTT
 A
 P F L V P G L G C Q D S P Q V A P P A P -
 b
 S F W F Q A L D A R I P R R L P R L P Q -
 c
 L S G S R P W M P G F P A G C P A C F S -
 GCGNACTGCGAATGCGGCGGCTTCTTCTGAGCTTCTTGGAAACCAAGCGGAGTGGCG
 1201 ----- 1260
 GCGNATACGCTTTAAGCGCGGCGGCAAGAGCTTCGACCAAGCTTGGTGGCGGCTACGCG
 A
 A * L A N A A P V S G A A W E P R A V P -
 b
 R Y W Q M R F L F L E L L G N H A Q C P -
 c
 P T G K C G P C F W S C L C T T R S A F -

Figure 72 (cont.)

CTACGGGTTTCTCTCAAGACCCACTGCCCCCTGCGAGCTGCGGTACCCCAAGCAGGCGG
 1261 ----- 1320
 CATGCCCCACAAGGAGTTCTGCGTGAAGGCGACGCTGAGGCCAGTGGGGTCTGCGGC
 a L R G V F Q D A L F A A S C G H P S S R -
 b Y G V F L K T H C P L R A A V T P A A G -
 c T G C S S R R T A R C E L R S P Q Q P V -
 TGTCTGTGCGCGGAGAGGCCCAAGGGCTCTGTGCGGCCCCCGAGGAGGAGGAACACAG
 1321 ----- 1380
 ACAGACACGGGCCCTCTTCTGGGGTCCCCGAGACACCGCCGGGGCTCTCTCTCTGTGTCT
 a C L C P G E A P G I C G G P R G G G T Q -
 b V C A K E K P Q G S V A A P E E E E H R -
 c S V P G R S P R A L W R P P R R E N T D -
 ACCCGGTGCGCTGCTGCGAGCTGCTCCGCGAGCAGCAGAGGCGCGGCGAGGTGTACGGCT
 1381 ----- 1440
 TGGGGCAGCGGACCACTGCGAGGCGGTCTGTCTGTCGAGGACCGTCCACATGCGGA
 a T P V A W C S C S A S T A A P G R C T A -
 b P P S P G A A A P P A Q Q P L A G V R L -
 c P R R L V Q L L R Q H S S P W Q V Y G F -
 TCGTGGGGCTGCGCTGCGCGCGCTGCTGCCCGAGGGCTCTGCGGCTCAGGACACAACG
 1441 ----- 1500
 AGCAGCGCGGAGCGAGCGCGCGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
 a S C G P A C A G W C P Q A S G A F G T T -
 b P A G L F A P A G A P R F L G I Q A Q R -
 c V R A C L R R L V P P G L W G S R H N E -
 AACGCGCGCTTCTCTAGGAACACCAAGAAGTTCATCTCTCTGCGGGAAGCATTCAGCTCT
 1501 ----- 1560
 TTGCGCGGAGGAGTCTCTGTGCTTCTCAACTAGACCGGACCTCTCTCTCTCTCTCTCTCT
 a N A A S S G T P R S S S P W G S M P S S -
 b T P L P Q E H Q E V H L P G E A C Q A L -
 c P R F L K N T K K F I S L G K H A E L S -
 CGCTGCGAGGCTGAGCTGGAAGATGAGGCTGCGGACTGCGGCTGCGGCTGCGGCTGCGGCT
 1561 ----- 1620
 GCGAGTCTCTGAGTCTGAGCTTCTACCTGCGAGGCGCTGAGCGGAACCGAGCGCTCTCTCT
 a R C R S * R G R * A C G T A L C C A G A -
 b A A G A D V E D E R A G L R L A A Q E P -
 c L Q E L T W K M S V R D C A W L R S P -
 CAGGCTTGGCTGTGTTCGGCGCGAGGCGACCGCTCTGCGTAGGAGATCTGCGGCAAGT
 1621 ----- 1680
 GTCCCGAACCAGACACAAGGCGCGGCTCTCTGTCGAGACCGCACTCTCTCTAGGAGCGGTCA
 a Q G L A V F R P Q S T V C V R R S W F S -
 b P G W L C S G R R A T S A * G D P G Q V -
 c G V G C V F A A E H R L R E E I L A K -

Figure 72 (cont.)

ACCGATATCCACAGGCGCTGSCCGACCTTGTGTCGCTGTGCGGTCAGGACCGCGCC
 2101 ----- 2160
 TGCTATAGGTGTCCCGGACCGCTGTGGAAGCAAGACGACACGCGCGGCTCTGCGCGCTG

 T I S T G P G A P S C C V C G P R T R -
 R Y F Q G L A H L R A A C A G P G P A A -
 D I H R A W R T F V L R V R A Q D P P P -

 CTCAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGCTACGACACCATCCCGCAGTACA
 2161 ----- 2220
 GACTCGACATGAACAGTTCCACGTACACTGCCCGCGCATGCTGTGTGTAGCGGCTCTGT

 L S C T L S R W M * R A P T T F S P R T -
 * A V L C Q G G C D G R V R H H P P G Q
 E L Y F V K V D V T G A Y D T I P Q D R -

 GCGTCACGGAGGTGATGCGCAGCATCATCAAAACCCAGAACAGTACTTCGCTGCTCGGT
 2221 ----- 2280
 CCGCATGCTCCAGTAGCGGTCTAGTAGTTTGGGCTCTTGTGATGACCGACGCGAGCA

 G S R R S S P A S S N P R T R T A C V G -
 A H G G H R Q H H Q T F E H V L R A S V -
 L T E V I A S I I K P Q N T Y C V R R Y -

 ATGCCGTGCTTCAGAACCGCCCATGCGCACGTCCGCAAGGCGCTTCAGAGGCAAGTCT
 2281 ----- 2340
 TACGCCACCAAGTCTTTCCCGCGGTACCGGTGACGGGCTTCGCGAAGTTCTTCGCTCAGA

 M P W S R R P P M G T S A R P E R A T S -
 C R G P E C R P W A R P Q G L Q E P R L -
 A V V Q K A A H G H V R K A F E S H V S

 CTACCTTCACAGACCTCCACCGCTACATCCACAGTCTGTGCTCAGCTTCAGGACAAACA
 2341 ----- 2400
 GATGGAAGTGTCTGAGGCTCGGATGTAGCTGTCTGACACCGAGTGTACGCTCTTCTGT

 L P * Q T S S R T C D S S W L T C R T -
 Y L D R P F A V H A T V R G S P A G ? Q -
 T L T D L Q P Y M R O F V A H L Q N S -

 GCGCCTGACCGCATCCCGTGTGATGAGCAGAGCTCTCTCCTGAAAGAGGCGACGATG
 2401 ----- 2460
 CGGCGGACTTCCCTACGGCAGCAGTAGCTCGTCTCGACGAGCGACTTACTTCGCTCTGAC

 A R * G M P E S S S R A P P * M R P A V -
 P A E G C R R H R A E L L P E * G Q Q W -
 P L R D A V V I E Q S S S L N E A S S G -

 GCGCTTTCACCGCTCTCTCTACGCTTCATGTCACACGCGCTCTGCGCTACAGGCGAAGT
 2461 ----- 2520
 CGGAGAGGCTGACAGAGGATGCGAAGTACACGGTGTGCGGACCGGTAGTTCGCGTCA

 A S S T S S Y A S C A T T P C A S G A S -
 P L R R L P T L H V P P R R A H Q G Q V -
 L F D V F L R F M C H H A V R I R G K S -

Figure 72 (cont.)

CCTACCTCCAGTCCACGCGGATCCCGCAGGCTCCATCTCTCCAGGCTGCTCTCCAGCC
 2521 ----- 2590
 GGATCCAGGTCACGCTCCCTAGGCGCTCCGAGGTAGGAGAGGTCGAGAGAGCTGG
 A T S S A R G S R R A P S S P R C S A A -
 L R P V P G D P A G L H F L H A A L Q F -
 Y V Q C C C I P Q G S I L S T L L C S L -
 TGTATACGGGACATGAGAACAAAGCTTTTCCGGGATTGCGGAGAGCGGCTGCTCC
 2581 ----- 2640
 AACATATTCGGCTGTACCTCTTTTTCGACAAACGCCCCCTAAGCGCGCCCTGCCCGAGGAG
 C A T A T W K T S C L R C F G G T C C S -
 V L R R H G E Q A V C G D S A G R A A P -
 C Y G D M E N K L F A G I R R D G L L L -
 TCCGTTTGGTGGAGCATTTCTTTCTTCTCAGACCTCAGCTCAGCCAGCGAAAACTTCC
 2641 ----- 2700
 ACGCAAAACCACTACTAAGAAGACACCACTCTGGAGTGGAGTGGGTCCTCTTTTGGAGG
 C V W W M I S C W * H L T S P T R K P S -
 A F G G * F L V G D T S P H T R E N L P -
 R L V D D F L L V T P H L T H A K T F L -
 TCAGGACCTTGGTCCAGCTCTCTCCTCAGTATGCTCTGCTGGAACCTTGGCGAAGACAG
 2701 ----- 2760
 AGTCTCTGGGACGAGGCTTCACAGGAGCTCATACGCAACCACTTCAAGGCTTTCTCTC
 S C P W S E V S L S M A A W * T C G R Q -
 Q D P G P R C P * V W I R G E L A E D S -
 F T L V R G V P E Y G C V V N L R K T V -
 TCGTCAACTTCTCTGTAGAAGACGAGGCGCTCTGCTCAGCGGCTTTTGTTCAGATGCGGG
 2761 ----- 2820
 ACCACTTGAAGGACATCTTCTGCTCCGGGACCCACCGTCCCGAAAACAATCTACGCTC
 W * T S L * K T R F W V A K L L P R C R -
 G E L P C R R R C P C W H G F C S D A G -
 V N F P V E D E A L G G T A F V Q M F A -
 CCCAGGCTTATTCCCTGCTCCGCGCTGCTCTGATACCGGACCTTGAAGCTCCAGA
 2821 ----- 2880
 GGCTCCGGATAAGGAGACTACGCTCGGACGAGGCTATGGGCTCTGGGACCTCCAGCTCT
 P T A Y S P G A A C C W I P C P W R C R -
 P R P I P L V R P A A G Y P D F G G A E -
 H G L F P W C G L L L C T R T L E V Q S -
 GCGACTACTCAGCTATCCCGGACCTCCATCAGAGCGACTCTCAGCTTCAACCGGCTT
 2881 ----- 2940
 CCTTATGAGGTCATACGGGCTCTGGAGCTAGTCTCTGCTCAGAGTGAAGTCTGGCGCA
 A T T P A M P G P P S E P V S P S T A A -
 R L L Q L C F D L H Q S Q S H L Q F R L -
 D Y S S Y A R T S I R A S L T F N R G P -

Figure 72 (cont.)

TDAAGGCTGGGAGGAACATGCTGCGAAACTTTTGGGGCTTTGGGGCTGAAGTGTGACA
 2941 ----- 3000
 AGTTGAGAGCTCTCTGTACGAGCGTTTGGAAACCGGAGAACCGGAGCTTACAGTGT

 S R L G G T C V A N S L G S C G * S V T
 Q G W E E H A S Q T L W G L A A E V S Q
 K A G R N M R R K L F G V I R L K C H S -

 GCTCTTTCTGTCATTTCACAGCTCAACAGCGCTGCAGAGCTGTGCACCAACATCTACAGA
 3001 ----- 3060
 CGGACAPAGAGCTTAAACGCTCCACITGTGCGAGGTCTCTCCACAGCTGGTGTAGATGTCT

 A C F W I C R * T A S K R C A F T S T K -
 P V S G F A G E Q F P D G V H Q H L Q D -
 L F L D L Q V N S L Q T V C T N I Y K I -

 TCTTCTGCTGCAAGGCTACAGGTTTCACAGCATGTGTCTGAGCTGCCATTTCATCAGC
 3061 ----- 3120
 AGGAGGACGAGCTCCGATGTCTCAAAGTGGTACACAGGCTGAGGCTTAAAGTAGTTC

 S S C C R R T G F T H V C C S S H F I S -
 P F A A G V Q V S R M C A A A P I S S A -
 L L L Q A Y R F H A C V L O L P F H O Q -

 AAGTTTGGAGAAACCCACATTTTCTGCGGCTCACTCTGACAGCGCTCTCTCTCTCT
 3121 ----- 3180
 TTCAACCTTCTTGGGGTGTAAAAACCGCCCACTACAGACTCTGCCCGAGCGGAGCGA

 K P G R T P H F S C A S S L T R P F S A -
 S L E E P H I F P A R H L * H G L P L L
 V W K N P T F F L R V I S D T A S L C Y

 ACTCCATCTCTAAAGCCCAACAACCGCAGGATCTCGCTGGGGGCTCAAGGGGCGGGCGGGG
 3181 ----- 3240
 TGAGTAGGACTTTCCTTCTTCTCTCTCTACAGCCAGCCCGCTTCCCGCGGGCGGGG

 T P S * K F R T Q G C E W G P R A F P A -
 L H F E S Q E R P D V A G G Q G R R R P -
 S I L K A K N A C M S L C A K C A A C P -

 CTCTGCTCTGGAGGCGCTGAGTGGCTGTGACCAAGCATTCCTGCTCAAGCTGACTC
 3241 ----- 3300
 GAGAGCGGAGGCTTCTGCGCAGCTACCCACAGCTGCTTCTTAAAGAGGCTTTCAGCTAG

 L C P P P P C S G C A T K H S C S S * L -
 S A L R G R A V A V P P S I P A Q A D S -
 L P S E A V Q W L C H Q A F L L K L T R -

 GACAGGCTGTACCTAGCTGCTCTCTGCGCTCACTTACGAGAGCGCTACAGCGAGCTTA
 3301 ----- 3360
 CTGTGTCACAGTGGATGACAGCTTACCGCCCACTGAGTCTCTCTCTCTCTCTCTCTCT

 D T V S P T C H S W G H S G Q F R R S * -
 T P C H L R A T P G V T Q D S P D A A E -
 H R V T Y V F L L G S L E T A Q T Q I S -

Figure 72 (cont.)

3361 GTGGGAAGCTCCCGGAGACGACCTGACTGCCCTGGAGGCGCGGAGCCAAACCGGACACTGG
 ----- 3420
 CAGCGTTCCAGGGCGCGCTGCTGGAGCTCAGCGGACCTCCCGGCTCGGCTGGCGGCTGACG

 A V G S S R G R R * L F W R P Q F T R H C -
 D E E A F G D D A D C P G G R S Q P G T A -
 C R K L F G T T L T A L E A A A N F A L P -

 3421 CCTGAGACTTCAGGACCATCTGGAGTGAATGCCACCTGCGCCACAGCCAGCCGAGAGCA
 ----- 3480
 GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGGCGGCTGTCCGCTCCCGCTCTCT

 A P Q T S R P S W T D G H F P T A R P R A -
 D L R L Q D H P G L H A T R P Q P G R E Q -
 C S D F K T I L D * W P F A H S Q A E S R -

 3481 GACACCAGCAGGCTCTCTCAAGCGGACTCTACGTCCCGAGGAGGGAGGGGGCGGCTCCACAC
 ----- 3540
 CTGTGCTGCTGGGACACTGCGCGCGAGATGCAGGGTCCCTTCCCTCCCGCGCGGTGTG

 A D T S S F V T P G S T S Q G G R G G P H -
 D T P A A L S R R A L K P R E G G A A H T -
 C H Q Q F C H A G L Y V P G R E G R F T F -

 3541 CCAGGCGCGGACCGGCTGGAGTCTCAAGGCTGAGTGAGTGTTTGGCGGAGGCTGCATGT
 ----- 3600
 GGTCCGGGCGTGGCGACCTCAGACTCCGACTCACTCACAACCGGCTCCGAGCTACA

 A F G P H R W E S E A * V S V W P R P A C -
 D Q A R T A G S L S P E * V F G R G L H V -
 C R P A P L G V * G L S E C L A E A C M S -

 3601 CCGGCTGAAGCTGAGTGTCTGGCTGAGGCTTACGCTAGTGTCCACCCACCGCTGAGTC
 ----- 3660
 GGCGACTTCCGACTCACAAGGCGACTCCGACTGCTCAGAGGTGCTTCCGACTTAC

 A P A E G * V S G * G L S E C P A K C * V -
 D R L F A E C P A E A * A S V Q P R A E C -
 C G * R L S V R L R P E R V S S Q G L S V -

 3661 TTCAGTACAGCTGCGCTCTTCACTTCCCGACAGCTGCGCTGCGCTCCACCCAGGGCT
 ----- 3720
 AGGTCTGTGGACGGGAGAACTGAAGCGCTGTCCGACCGGAGCGGAGGTGGGCTCCG

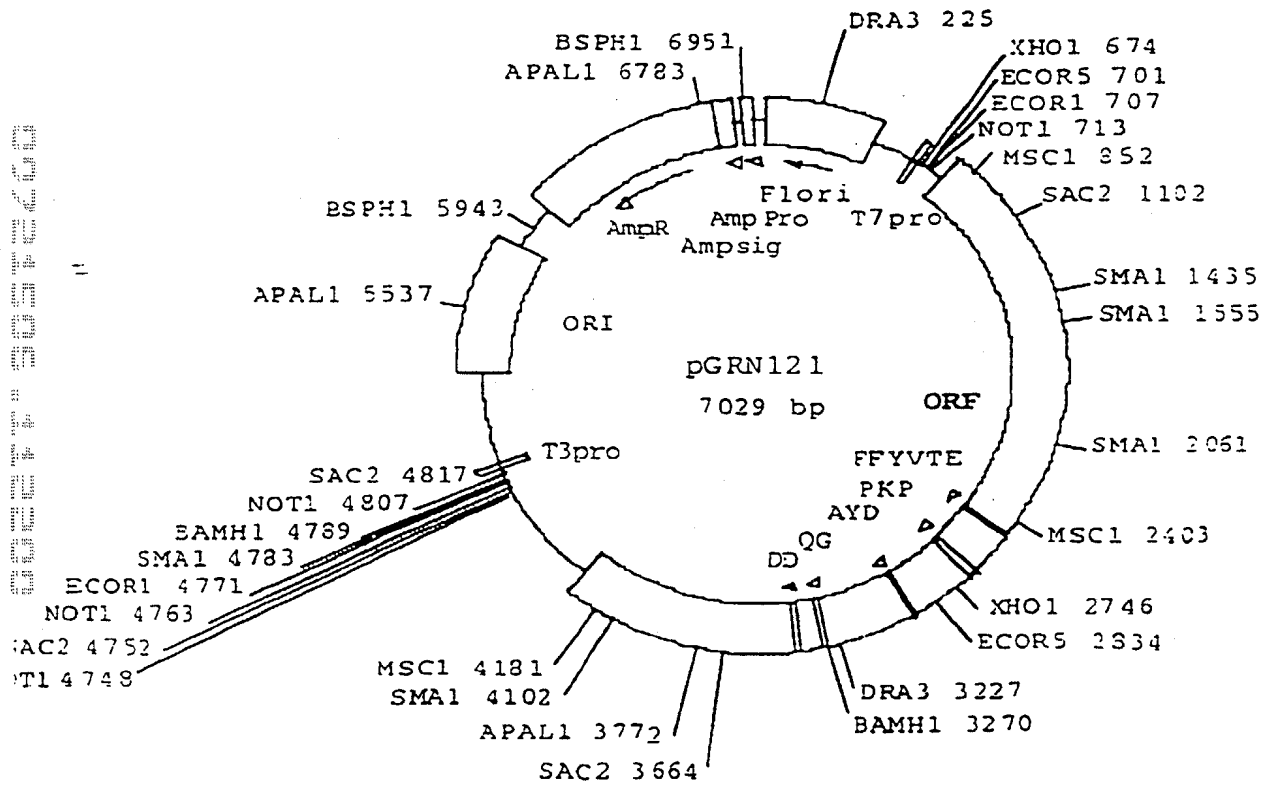
 A S S T P A V F T S P Q A G A R I H P R A -
 D P A H L P S S L P H R L A L G S T P G P -
 C Q H T C R L H F P T G W R S A P P Q G Q -

 3721 AGCTTTTCTCAGCAGGAGCGCGGCTTCACTCCCGACATAGGAATAGTTCATCCCGAGA
 ----- 3780
 TCGAAGGAGTGTCTCTCGGCGGAGGCTAGGGGTGTAATCTTATCACTAGCGGCTCT

 A S F S S P G A R L P L P T * E * S T P R
 D A P P H Q E F G F H S P H R N S P S P D -
 C L F L T R S P A S T P H I G I V H F Q T -

00924506 443000

Figure 73



1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACC TTC GTG CGG CGC CTG

30
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

50
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

80
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

100
120
130

Figure 74 (cont.)

			290										300		
gly	ala	leu	ser	gly	thr	arg	his	ser	his	pro	ser	val	gly	arg	
GGT	GCG	CTC	TCT	GGC	ACG	CGC	CAC	TCC	CAC	CCA	TCC	GTG	GGC	CGC	
								310							
gln	his	his	ala	gly	pro	pro	ser	thr	ser	arg	pro	pro	arg	pro	
CAG	CAC	CAC	GCG	GGC	CCC	CCA	TCC	ACA	TCG	CGG	CCA	CCA	CGT	CCC	
			320										330		
trp	asp	thr	pro	cys	pro	pro	val	tyr	ala	glu	thr	lys	his	phe	
TGG	GAC	ACG	CCT	TGT	CCC	CCG	GTG	TAC	GCC	GAG	ACC	AAG	CAC	TTC	
								340							
leu	tyr	ser	ser	gly	asp	lys	glu	gln	leu	arg	pro	ser	phe	leu	
CTC	TAC	TCC	TCA	GGC	GAC	AAG	GAG	CAG	CTG	CGG	CCC	TCC	TTC	CTA	
			350										360		
leu	ser	ser	leu	arg	pro	ser	leu	thr	gly	ala	arg	arg	leu	val	
CTC	AGC	TCT	CTG	AGG	CCC	AGC	CTG	ACT	GGC	GCT	CGG	AGG	CTC	GTG	
								370							
glu	thr	ile	phe	leu	gly	ser	arg	pro	trp	met	pro	gly	thr	pro	
GAG	ACC	ATC	TTT	CTG	GGT	TCC	AGG	CCC	TGG	ATG	CCA	GGG	ACT	CCC	
			380										390		
arg	arg	leu	pro	arg	leu	pro	gln	arg	tyr	trp	gln	met	arg	pro	
CGC	AGG	TTG	CCC	CGC	CTG	CCC	CAG	CGC	TAC	TGG	CAA	ATG	CGG	CCC	
								400							
leu	phe	leu	glu	leu	leu	gly	asn	his	ala	gln	cys	pro	tyr	gly	
CTG	TTT	CTG	GAG	CTG	CTT	GGG	AAC	CAC	GCG	CAG	TGC	CCC	TAC	GGG	
			410										420		
val	leu	leu	lys	thr	his	cys	pro	leu	arg	ala	ala	val	thr	pro	
GTG	CTC	CTC	AAG	ACG	CAC	TGC	CCG	CTG	CGA	GCT	GCG	GTC	ACC	CCA	
								430							
ala	ala	gly	val	cys	ala	arg	glu	lys	pro	gln	gly	ser	val	ala	
GCA	GCC	GGT	GTC	TGT	GCC	CGG	GAG	AAG	CCC	CAG	GCC	TCT	GTG	GCG	

Figure 74 (cont.)

440 450
 ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
 GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
 leu arg gln his ser ser pro trp gln val tyr gly phe val arg
 CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
 ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
 GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
 his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
 CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
 leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
 CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
 met ser val arg asp cys ala trp leu arg arg ser pro gly val
 ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
 gly cys val pro ala ala glu his arg leu arg glu glu ile leu
 GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
 ala lys phe leu his trp leu met ser val tyr val val glu leu
 GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
 leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
 CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACC TTT CAA AAG AAC

580
 arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
 AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
 ile gly ile arg gln his leu lys arg val gln leu arg glu leu
 ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

Figure 74 (cont.)

														610
ser	glu	ala	glu	val	arg	gln	his	arg	glu	ala	arg	pro	ala	leu
TCG	GAA	GCA	GAG	GTC	AGG	CAG	CAT	CGG	GAA	GCC	AGG	CCC	GCC	CTG
														620
leu	thr	ser	arg	leu	arg	phe	ile	pro	lys	pro	asp	gly	leu	arg
CTG	ACG	TCC	AGA	CTC	CGC	TTC	ATC	CCC	AAG	CCT	GAC	GGG	CTG	CGG
														630
														640
pro	ile	val	asn	met	asp	tyr	val	val	gly	ala	arg	thr	phe	arg
CCG	ATT	GTG	AAC	ATG	GAC	TAC	GTC	GTG	GGA	GCC	AGA	ACG	FTC	CGC
														650
arg	glu	lys	arg	ala	glu	arg	leu	thr	ser	arg	val	lys	ala	leu
AGA	GAA	AAG	AGG	GCC	GAG	CGT	CTC	ACC	TCG	AGG	GTG	AAG	GCA	CTG
														660
														670
phe	ser	val	leu	asn	tyr	glu	arg	ala	arg	arg	pro	gly	leu	leu
TTC	AGC	GTG	CTC	AAC	TAC	GAG	CGG	GCG	CGG	CGC	CCC	GGC	CTC	CTG
														680
gly	ala	ser	val	leu	gly	leu	asp	asp	ile	his	arg	ala	trp	arg
GGC	GCC	TCT	GTG	CTG	GGC	CTG	GAC	GAT	ATC	CAC	AGG	GCC	TGG	CGC
														690
														700
thr	phe	val	leu	arg	val	arg	ala	gln	asp	pro	pro	pro	glu	leu
ACC	TTC	GTG	CTG	CGT	GTG	CGG	GCC	CAG	GAC	CCG	CCG	CCT	GAG	CTG
														710
tyr	phe	val	lys	val	asp	val	thr	gly	ala	tyr	asp	thr	ile	pro
TAC	TTT	GTC	AAG	GTG	GAT	GTG	ACG	GGC	GCG	TAC	GAC	ACC	ATC	CCC
														720
														730
gln	asp	arg	leu	thr	glu	val	ile	ala	ser	ile	ile	lys	pro	gln
CAG	GAC	AGG	CTC	ACG	GAG	GTC	ATC	GCC	AGC	ATC	ATC	AAA	CCC	CAG
														740
asn	thr	tyr	cys	val	arg	arg	tyr	ala	val	val	gln	lys	ala	ala
AAC	ACG	TAC	TGC	GTG	CGT	CGG	TAT	GCC	GTG	GTC	CAG	AAG	GCC	GCC
														750
														760
his	gly	his	val	arg	lys	ala	phe	lys	ser	his	val	ser	thr	leu
CAT	GGG	CAC	GTC	CGC	AAG	GCC	TTC	AAG	AGC	CAC	GTC	TCT	ACC	TTG

Figure 74 (cont.)

770														780	
thr	asp	leu	gln	pro	tyr	met	arg	gln	phe	val	ala	his	leu	gln	
ACA	GAC	CTC	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	
790															
glu	thr	ser	pro	leu	arg	asp	ala	val	val	ile	glu	gln	ser	ser	
GAG	ACC	AGC	CCG	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	
800														810	
ser	leu	asn	glu	ala	ser	ser	gly	leu	phe	asp	val	phe	leu	arg	
TCC	CTG	AAT	GAG	GCC	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	
820															
phe	met	cys	his	his	ala	val	arg	ile	arg	gly	lys	ser	tyr	val	
TTC	ATG	TGC	CAC	CAC	GCC	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	
830														840	
gln	cys	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	
CAG	TGC	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	
850															
cys	ser	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	
TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	
860														870	
ile	arg	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	
ATT	CGG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	
880															
leu	val	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	
TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	
890														900	
leu	val	arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	
CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	
910															
lys	thr	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	
AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GCG	
920														930	
thr	ala	phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	
ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	

Figure 74 (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CCG ACC CTG GAG GTG CAG AGC GAC TAC

950 960
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CCG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

970
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

980 990
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CCG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

1000
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1010 1020
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040 1050
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GCG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1070 1080
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

Figure 74 (cont.)

1100 1110
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG
 1120
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
 CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC
 1130 1132
 phe lys thr ile leu asp OP
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCCCACAGCCAGGCCGAGAGCAGA
 CACCAGCAGCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGCCCCACACCC
 AGGCCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGCCCCAGGCCTGCATGTCC
 GGCTGAAGGCTGAGTGTCGGCTGAGGCCTGAGCGAGTGTCAGCCAAGGGCTGAGTGTC
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
 CTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
 CGCCATTGTTACCCCTGCCCCTGCCCTTTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA
 GACCCTGAGAAGGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
 CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTCGGGGGAGGTGC
 TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTTGRAAAAAAAAAAAAAAAAAA
 AAAAAAAAAA

Figure 75

KPN1 17050
KPN1 18560
ECOR1 19475
SAC1 19652
SAC1 21083
ECOR1 22539
SAC1 24607
SAC1 29043

<-TCP